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OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 18:13:48 ; Search time 13687 Seconds
(without alignments)
11466.729 Million cell updates/sec

Title: US-10-045-072-1
Perfect score: 3621
Sequence: 1 tggggcggggttagatcctg.....tgatcgtcgtcttctctaa 3621

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
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- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3621	100.0	3621	6	AR123974	AR123974 Sequence
2	3621	100.0	3621	6	AR213173	AR213173 Sequence
3	3621	100.0	3637	1	AF038548	AF038548 Coryneb
4	3621	100.0	332050	1	AP005276	AP005276 Coryneb
5	3621	100.0	349980	6	AX127145	AX127145 Sequence
6	3578	98.8	3728	1	CGPYC	Y09548 Corynebacte
7	3578	98.8	3728	6	A97276	A97276 Sequence 1
8	3578	98.8	3728	6	BD140686	BD140686 Method fo
9	3469	95.8	3657	1	AF503915	AF503915 Coryneb
10	3420	94.4	3420	6	AX120849	AX120849 Sequence
11	3420	94.4	3420	6	BD162966	BD162966 Novel pol
12	3398.8	93.9	3474	6	AX453601	AX453601 Sequence
13	3398.8	93.9	3474	6	AX453603	AX453603 Sequence
14	2282.8	63.0	308750	1	AP005216	AP005216 Coryneb
15	2279.6	63.0	4013	6	BD094153	BD094153 Genes for
16	2279.6	63.0	4851	1	AB083299	AB083299 Coryneb
17	1927.4	53.2	341553	1	BX248355	BX248355 Coryneb
18	1708	47.2	1719	6	AX064993	AX064993 Sequence
19	1395	38.5	1406	6	AX064995	AX064995 Sequence
20	1344.6	37.1	291000	1	SCO939105	AL939105 Streptomy
21	1328.2	36.7	4218	1	AF262949	AF262949 Mycobacte
22	1294.4	35.7	17992	1	AE007125	AE007125 Mycobacte
23	1294.4	35.7	348676	15	BX842581	BX842581 Mycobacte
24	1292.8	35.7	318050	1	BX248344	BX248344 Mycobacte
25	1249.6	34.5	31175	1	MTU00024	U00024 Mycobacteri
26	1249.6	34.5	31176	1	MSGY2	AD000009 Mycobacte
27	1249.6	34.5	32155	6	AR345347	AR345347 Sequence
28	1033	28.5	1083	6	AX064989	AX064989 Sequence
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30	907	25.0	939	6	AX064985	AX064985 Sequence
31	907	25.0	939	6	AX064987	AX064987 Sequence
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33	899	24.8	324227	1	AE016852	AE016852 Tropherym
34	741.4	20.5	303862	1	AE017215	AE017215 Geobacter
35	720	19.9	4010	5	AB086371	AB086371 Pagrus ma
36	714	19.7	3994	4	AY185595	AY185595 Bos tauru
37	707.8	19.5	3537	4	AY225510	AY225510 Sus scrof
38	705.4	19.5	347786	1	BX640438	BX640438 Bordetell
39	703.2	19.4	3916	8	AF097728	AF097728 Aspergill
40	701.2	19.4	3559	5	AF509529	AF509529 Gallus ga
41	699	19.3	349146	1	BX640424	BX640424 Bordetell
42	691.8	19.1	3953	9	HSU04641	U04641 Human pyruv
43	691.8	19.1	4049	9	BC011617	BC011617 Homo sapi
44	690.6	19.1	4067	10	MUSMPYR	L09192 Mus musculu
45	690.2	19.1	3960	9	HSU30891	U30891 Human pyruv

ALIGNMENTS

RESULT 1	AR123974	AR123974	3621 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	Sequence 1	from patent US 6171833.				
DEFINITION	Sequence 1	from patent US 6171833.				
ACCESSION	AR123974					
VERSION	AR123974.1	GI:14109335				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 3621)					
AUTHORS	Sinskey,A.J., Lessard,P.A. and Willis,L.B.					
TITLE	Pyruvate carboxylase from corynebacterium glutamicum					
JOURNAL	Patent: US 6171833-A 1 09-JAN-2001;					
FEATURES	Location/Qualifiers					

source	1. .3621
ORIGIN	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	100.0%; Score 3621; DB 6; Length 3621;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 3621; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 TGGGGCGGGTTAGATCCTCGGGGTTTTATTTCATTCACTTGGCTTGAAGTCGTGCAGG 60
DB	1 TGGGGCGGGTTAGATCCTCGGGGTTTTATTTCATTCACTTGGCTTGAAGTCGTGCAGG 60
QY	61 TCAGGGGAGTGTTGCCCGAATAACATTGAGAGGAAAAACAATAAACCCGATGTTTGTATGGGGG 120
DB	61 TCAGGGGAGTGTTGCCCGAATAACATTGAGAGGAAAAACAATAAACCCGATGTTTGTATGGGGG 120
QY	121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCCTGGCGGTCTCTTTGTTG 180
DB	121 AATCGGGGGTTACGATACTAGGACGCAGTGACTGCTATCACCCCTGGCGGTCTCTTTGTTG 180
QY	181 AAAGGAATAATTACTCTAGTGTGCACTCACACATCTTCAAACGCTTCCAGCATTCAAAAAG 240
DB	181 AAAGGAATAATTACTCTAGTGTGCACTCACACATCTTCAAACGCTTCCAGCATTCAAAAAG 240
QY	241 ATCTTGGTAGCAAAACCGCGGCGAAATCGCGGTCCGTGCTTTCGTGTCAGCACTCGAAACC 300
DB	241 ATCTTGGTAGCAAAACCGCGGCGAAATCGCGGTCCGTGCTTTCGTGTCAGCACTCGAAACC 300
QY	301 GGTGAGCCACGGTAGCTATTTACCCCCTGGAAGATCGGGGATCAATCCACCGCTCTTTT 360
DB	301 GGTGAGCCACGGTAGCTATTTACCCCCTGGAAGATCGGGGATCAATCCACCGCTCTTTT 360
QY	361 GCTTCTGAAGCTGTCCGATTTGTAACCGAAGGCTCACCCAGTCAAGGCGTACCTGGACATC 420
DB	361 GCTTCTGAAGCTGTCCGATTTGTAACCGAAGGCTCACCCAGTCAAGGCGTACCTGGACATC 420
QY	421 GATGAAATTTATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480
DB	421 GATGAAATTTATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480
QY	481 TTCTCTGTGAAAATGCCAGCTTGCCCGGAGTGTGCGGAAAAACGGCATTACTTTTATT 540
DB	481 TTCTCTGTGAAAATGCCAGCTTGCCCGGAGTGTGCGGAAAAACGGCATTACTTTTATT 540
QY	541 GGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGTAAACCGCCGCG 600
DB	541 GGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGTAAACCGCCGCG 600
QY	601 AAGAAGCTGGTCTGCCAGTTTTCGGGAATCCACCCGAGCAAAAACATCGATGAGATC 660
DB	601 AAGAAGCTGGTCTGCCAGTTTTCGGGAATCCACCCGAGCAAAAACATCGATGAGATC 660
QY	661 GTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720
DB	661 GTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGGTGGTGGC 720
QY	721 GGACGCGGTATGCGTTTGTGTGCTTCACTGATGAGCTTCGCAATTAGCAACAGAAAGCA 780
DB	721 GGACGCGGTATGCGTTTGTGTGCTTCACTGATGAGCTTCGCAATTAGCAACAGAAAGCA 780
QY	781 TCTCGTGAAGCTGAAGCGGCTTTTCGGCGATGGCGGGTATATGTCGAACGTGTGTGATT 840
DB	781 TCTCGTGAAGCTGAAGCGGCTTTTCGGCGATGGCGGGTATATGTCGAACGTGTGTGATT 840
QY	841 AACCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAAGTTGTACACCTT 900
DB	841 AACCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAAGTTGTACACCTT 900
QY	901 TATGAACGTGACTGCTCACTGCAGCGTGTGTCACCAAAAAGTTGTGCAATTCGCCAGCA 960
DB	901 TATGAACGTGACTGCTCACTGCAGCGTGTGTCACCAAAAAGTTGTGCAATTCGCCAGCA 960

QY	961	CAGCA	TTTGGATCCAGAACTCGGTGATCGCATTTGTGCGGATGAGTAAAGTTCTCTGCCGC	1020
DB	961	CAGCA	TTTGGATCCAGAACTCGGTGATCGCATTTGTGCGGATGAGTAAAGTTCTCTGCCGC	1020
QY	1021	TCCATTGGTTAC	CAGGGCGGGAAACCGTGGAAATCTTGGTCGATGAAAGGGCAACCCAC	1080
DB	1021	TCCATTGGTTAC	CAGGGCGGGAAACCGTGGAAATCTTGGTCGATGAAAGGGCAACCCAC	1080
QY	1081	GTCTTCATCGAAATGA	ACCCACGATCCAGGTTGAGCACACCGTGACTGAAGAAAGTCACC	1140
DB	1081	GTCTTCATCGAAATGA	ACCCACGATCCAGGTTGAGCACACCGTGACTGAAGAAAGTCACC	1140
QY	1141	GAGGTGGACCTGGTGA	AGGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG	1200
DB	1141	GAGGTGGACCTGGTGA	AGGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG	1200
QY	1201	GGTCTGACCCAAAGATA	GAAGATCAAGACCCACGGTGACGACTGCAGTGCGGCATCACCCAG	1260
DB	1201	GGTCTGACCCAAAGATA	GAAGATCAAGACCCACGGTGACGACTGCAGTGCGGCATCACCCAG	1260
QY	1261	GAAGATCCAAACAAACGGCTT	CCGCCACAGATACCGGAACCTATCACCGGTACCGCTCACCA	1320
DB	1261	GAAGATCCAAACAAACGGCTT	CCGCCACAGATACCGGAACCTATCACCGGTACCGCTCACCA	1320
QY	1321	GGCGGAGCTGGCGTT	CGTCTTGACGGTGACGCTCAGCTCGGTGGGAAATCACCGGCATCACCGCACAC	1380
DB	1321	GGCGGAGCTGGCGTT	CGTCTTGACGGTGACGCTCAGCTCGGTGGGAAATCACCGGCATCACCGCACAC	1380
QY	1381	TTTGACTCCATGCTGGTGAA	AAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTGCT	1440
DB	1381	TTTGACTCCATGCTGGTGAA	AAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTGCT	1440
QY	1441	CGTGCA	CAGCGCGTTGGCTGAGTTCAACCGTGCTGGTGGCAACCAACATTGGTTTC	1500
DB	1441	CGTGCA	CAGCGCGTTGGCTGAGTTCAACCGTGCTGGTGGCAACCAACATTGGTTTC	1500
QY	1501	TTGCGTGCGTTGCTGCGG	GAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT	1560
DB	1501	TTGCGTGCGTTGCTGCGG	GAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT	1560
QY	1561	GCCGATCACCCGCACTCCTT	CAGGCTCCACTGCTGATGATGAGCAGGACGCGATCCTGT	1620
DB	1561	GCCGATCACCCGCACTCCTT	CAGGCTCCACTGCTGATGATGAGCAGGACGCGATCCTGT	1620
QY	1621	GATTACTTGGCAGATGT	CACCGTGAAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA	1680
DB	1621	GATTACTTGGCAGATGT	CACCGTGAAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA	1680
QY	1681	GCTCCTATCGATAAGCTG	CCTAAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC	1740
DB	1681	GCTCCTATCGATAAGCTG	CCTAAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC	1740
QY	1741	CGCCTGAAGCAGCTTGG	CCAGCCGATCTCCGTGAGCAGGACGCACTG	1800
DB	1741	CGCCTGAAGCAGCTTGG	CCAGCCGATCTCCGTGAGCAGGACGCACTG	1800
QY	1801	GCAGTTACTGATACCACTT	CCGCGATGCACACCACTTCTGCTTGCACCCGAGTCGCG	1860
DB	1801	GCAGTTACTGATACCACTT	CCGCGATGCACACCACTTCTGCTTGCACCCGAGTCGCG	1860
QY	1861	TCATTGCACTGAAGCCT	TGCGGCAGAGCCGTCGCAAGAGTGACTCCTGAGCTTTTGTC	1920
DB	1861	TCATTGCACTGAAGCCT	TGCGGCAGAGCCGTCGCAAGAGTGACTCCTGAGCTTTTGTC	1920
QY	1921	GTGGAGGCCTGGGGCG	CGACCTACGATGTGGCGATGCTTCTCTTTTGAGGATCCG	1980
DB	1921	GTGGAGGCCTGGGGCG	CGACCTACGATGTGGCGATGCTTCTCTTTTGAGGATCCG	1980
QY	1981	TGGGACAGGCTCGACG	AGCTGCGCGAGGCGATGCCGAATGTAAACATTTCAGATGCTGCTT	2040
DB	1981	TGGGACAGGCTCGACG	AGCTGCGCGAGGCGATGCCGAATGTAAACATTTCAGATGCTGCTT	2040
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QY 2101 AAGGAAGCTGCCAGCTCCGGCTGGACATCTTCGACATCTTCGACGCGCTTAACGACGTC 2160
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QY 2161 TCCAGATGCGTCCAGCAATCGACGAGTCTCTGATCCAAATGAAAAGCTCTACACCCCTGGATTAC 2220
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QY 2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAAGAT 2340
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Db 3541 |||||GTTGACGGCAAAATCGATCGCTGTTGTGTTCTCTGCTCAACGAAGTGAAGTGGCGAC 3600
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RESULT 2
AR213173
LOCUS AR213173 3621 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 1 from patent US 6403351.
ACCESSION AR213173
VERSION AR213173.1 GI:23310240
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3621)
AUTHORS Sinskey,A.J., Lessard,P.A. and Willis,L.B.
TITLE Pyruvate carboxylase polypeptide from Corynebacterium glutamicum
JOURNAL Patent: US 6403351-A 1 11-JUN-2002;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 3621; DB 6; Length 3621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TCAGGGGAGTGTTCGCCGAAACATTTGAGAGGAAACAAAACCGATGTTTGTATGGGG 120
Db 61 TCAGGGGAGTGTTCGCCGAAACATTTGAGAGGAAACAAAACCGATGTTTGTATGGGG 120
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|||||

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Qy 901 TATGAACGTGACTGCTCACTGACGCTCGTCAACAAAAGTTGTGAAATTTGCCGAGCA 960
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ACCESSION AF038548
VERSION AF038548.1 GI:2708716
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ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE 1 (bases 1 to 3637)
AUTHORS Koffas,M.A., Ramamoorthi,R., Pine,W.A., Sinskey,A.J. and
Stephanopoulos,G.
TITLE Sequence of the Corynebacterium glutamicum pyruvate carboxylase
gene
JOURNAL Appl. Microbiol. Biotechnol. 50 (3), 346-352 (1998)
MEDLINE 99019028
PUBMED 9802220
REFERENCE 2 (bases 1 to 3637)
AUTHORS Koffas,M.A.G., Ramamoorthi,R., Pine,W.A., Sinskey,A.J. and
Stephanopoulos,G.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1997) Chemical Engineering, Massachusetts
Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA
02139, USA
FEATURES
Location/Qualifiers
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RESULT 4

AP005276

LOCUS

DEFINITION

AP005276 332050 bp DNA linear BCT 08-AUG-2002
Corynebacterium glutamicum ATCC 13032 DNA, complete genome, section 3/10.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AP005276 BA000036

AP005276.1 GI:21323419

Corynebacterium glutamicum ATCC 13032

Corynebacterium glutamicum ATCC 13032

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

1

Nakagawa,S.

Complete genomic sequence of Corynebacterium glutamicum ATCC 13032

Unpublished

2 (bases 1 to 332050)

Nakagawa,S.

Direct Submission

Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co.

Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,

Tokyo 194-8533, Japan (E-mail:snakagawa@xanagen.com,

Tel:81-44-829-3031, Fax:81-44-813-1651)

This sequence is conducted by collaboration of Kyowa Hakko Kogyo

Co. Ltd. And Kitasato University.

COMMENT

FEATURES

source

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RESULT 5
AX127145

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KEYWORDS	.
SOURCE	Corynebacterium glutamicum
ORGANISM	Corynebacterium glutamicum
	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE AUTHORS

REFERENCES	1
AUTHORS	Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
TITLE	Novel polynucleotides
JOURNAL	Patent: EP 1108790-A 7061 20-JUN-2001;

FEATURES
SOURCE

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ORIGIN

Query Match									
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RESULT 6

CGPYC
LOCUS Corynebacterium glutamicum pyc gene.
DEFINITION Corynebacterium glutamicum pyc gene.
ACCESSION Y09548
VERSION Y09548.1 GI:2879822
KEYWORDS pyc gene; pyruvate carboxylase.
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE 1
AUTHORS Peters-Wendisch,P.G., Kreutzer,C., Kalinowski,J., Patek,M., Sahm,H.
and Eikmanns,B.J.
TITLE Pyruvate carboxylase from Corynebacterium glutamicum:
characterization, expression and inactivation of the pyc gene
JOURNAL Microbiology (Reading, Engl.) 144 (Pt 4), 915-927 (1998)
MEDLINE 98240228
PUBMED 9579065
REFERENCE 2 (bases 1 to 3728)
AUTHORS Peters-Wendisch,P.G.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-1996) P.G. Peters-Wendisch, Institut fuer
Biotechnologie 1, Forschungszentrum Juelich GmbH, Juelich, D-52425,
FRG

FEATURES
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ORIGIN

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Matches 3578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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A97276 LOCUS A97276 3728 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 1 from Patent WO9918228.

ACCESSION A97276

VERSION A97276.1 GI:6780661

KEYWORDS

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 3728)

AUTHORS Peters-Wendisch,P. and Eikmanns,B.

TITLE METHOD FOR MICROBIAL PRODUCTION OF AMINO ACIDS OF THE ASPARTATE

JOURNAL AND/OR GLUTAMATE FAMILY AND AGENTS WHICH CAN BE USED IN SAID METHOD

Patent: WO 9918228-A 1 15-APR-1999;

PETERS WENDISCH PETRA (DE); EIKMANNS BERND (DE)

FEATURES Location/Qualifiers

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ORIGIN

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BD140686 3728 bp DNA linear PAT 18-SEP-2002
LOCUS Method for microbial production of amino acids of the aspartate
DEFINITION and/or glutamate family and agents which can be used in said
method.

ACCESSION BD140686
VERSION BD140686.1 GI:232335631
KEYWORDS JP 2002508921-A/1.
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum

REFERENCE 1 (bases 1 to 3728)
AUTHORS Eikmanns,B., Wendisch,P.P. and Sahm,H.
TITLE Method for microbial production of amino acids of the aspartate

JOURNAL and/or glutamate family and agents which can be used in said method
COMMENT Patent: JP 2002508921-A 1 26-MAR-2002;
FORSCHUNGSZENTRUM JULICH GMBH
OS Corynebacterium glutamicum
PN JP 2002508921-A/1
PD 26-MAR-2002
PF 30-SEP-1998 JP 2000515022
PR 04-OCT-1997 DE 197 43 894.6,14-JUL-1998 DE 198 31 609.7 PI

BERND EIKMANNs,PETRA PETERS WENDISCH,HERMANN SAHM PC
C12N15/09,C12N1/21,C12P13/20//(C12P13/20,C12R1:15),C12N15/00 CC
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FH Key Location/Qualifiers
FT CDS (165)..(3587).

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ORIGIN
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Matches 3578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 130 TTGGCGGTCTCTTTGTTGAAGGAATAATTACTTAGTGTGACTCACACATCTTCAACGC 189

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RESULT 9
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DEFINITION Corynebacterium crenatum strain CD945 pyruvate carboxylase (pyc)
gene, complete cds.
ACCESSION AF503915
VERSION AF503915.1 GI:20531756
KEYWORDS
SOURCE Corynebacterium crenatum
ORGANISM Corynebacterium crenatum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE 1 (bases 1 to 3657)
AUTHORS Wang, J., Ding, J. and Liu, Y.
TITLE Cloning and Expression of Pyruvate Carboxylase Gene in Corynebacterium crenatum CD945
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3657)
AUTHORS Wang, J., Ding, J. and Liu, Y.
TITLE Direct Submission
JOURNAL Submitted (18-APR-2002) Center of Microbial Biotechnology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100080, China

FEATURES
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RESULT 10
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LOCUS          3420 bp          linear          PAT 11-M
DEFINITION    Sequence 765 from Patent EP1108790.
ACCESSION     AX120849
VERSION       AX120849.1  GI:14037564
KEYWORDS
SOURCE        Corynebacterium glutamicum
ORGANISM      Corynebacterium glutamicum
               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
               Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1
REFERENCE     1
AUTHORS       Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
               Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
TITLE         Novel polynucleotides
JOURNAL       Patent: EP 1108790-A 765 20-JUN-2001;
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FEATURES      Location/Qualifiers
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SOURCE
ORIGIN

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Query Match 94.4%; Score 3420; DB 6; Length 3420;
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LOCUS BD162966 3420 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel polynucleotide.
ACCESSION BD162966
VERSION BD162966.1 Gr:27868728

KEYWORDS JP 2002191370-A/765.
SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified.
AUTHORS 1 (bases 1 to 3420)
Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,A.
TITLE Novel polynucleotide
JOURNAL Patent: JP 2002191370-A 765 09-JUL-2002;
KYOWA HAKKO KOGYO CO LTD
COMMENT OS Corynebacterium glutamicum
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PF 15-DEC-2000 JP 2000405096
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PI KEIKO OCHIAI,
PI HARUHIKO YOKOI,NAOKO TATEISHI,AKIHIRO SENOO,NASATO IKEDA,AKIO
PI OZAKI
PC C12N15/09,C12N15/09,C07K14/34,C07K16/12,C07K16/40,C12M1/00,PC
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DEFINITION Sequence 1 from Patent WO0231158.
ACCESSION AX453601
VERSION AX453601.1 GI:21712841
KEYWORDS
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE 1
AUTHORS Hanke, P.D.
TITLE Feedback-resistant pyruvate carboxylase gene from corynebacterium
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ORIGIN

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ACCESSION AX453603
VERSION AX453603.1 GI:21712843
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REFERENCE 1
AUTHORS Hanke, P.D.
TITLE Feedback-resistant pyruvate carboxylase gene from corynebacterium
JOURNAL Patent: WO 0231158-A 3 18-APR-2002;
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RESULT 15

BD094153

LOCUS

DEFINITION Genes for heat resistant enzymes of amino acid biosynthetic pathway derived from thermophilic coryneform bacteria.

ACCESSION BD094153

VERSION BD094153.1 GI:22639741

KEYWORDS WO 0125447-A/11.

SOURCE Corynebacterium thermoaminogenes

ORGANISM Corynebacterium thermoaminogenes

REFERENCE 1 (bases 1 to 4013)

AUTHORS Hirano,S., Nonaka,G., Matsuzaki,Y., Akiyoshi,N., Nakamura,K., Kimura,E., Osumi,T., Matsui,K., Kawahara,Y., Kurahashi,O., Nakamatsu,T. and Sugimoto,S.

TITLE Genes for heat resistant enzymes of amino acid biosynthetic pathway derived from thermophilic coryneform bacteria

JOURNAL Patent: WO 0125447-A 11 12-APR-2001; AJINOMOTO CO INC SEIKO HIRANO,GEN NONAKA,YUMI MATSUZAKI, NAOKI AKIYOSHI, KANAE NAKAMURA,EIICHIRO KIMURA,TSUYOSHI OSUMI,KAZUHIKO MATSUI, YOSHIO KAWAHARA,OSAMU KURAHASHI,TSUYOSHI NAKAMATSU, SHINICHI SUGIMOTO

COMMENT OS Corynebacterium thermoaminogenes

PN WO 0125447-A/11

PD 12-APR-2001

PF 04-OCT-2000 WO 2000JP006913

PR 04-OCT-1999 JP 99P 282716,01-NOV-1999 JP 99P 311147 PR 21-APR-2000 JP 00P 120687

PI SEIKO HIRANO,GEN NONAKA,YUMI MATSUZAKI,NAOKI AKIYOSHI,KANAE NAKAMURA,

PI EIICHIRO KIMURA,TSUYOSHI OSUMI,KAZUHIKO

PI OSAMU KURAHASHI,TSUYOSHI NAKAMATSU,SHINICHI SUGIMOTO PC C12N15/60,C12N15/54,C12N15/53,C12N15/31,C12N15/56,C12N9/88, PC C12N9/12,

PC C12N9/04,C07K14/34,C12N9/26,C12N13/04

CC

Key Location/Qualifiers

Key CDS (319)..(3735).

FT Location/Qualifiers

source 1..4013

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/db_xref="taxon:161484"

ORIGIN

Query Match 63.0%; Score 2279.6; DB 6; Length 4013;

Best Local Similarity 77.7%; Pred.No. 0;

Matches 2808; Conservative 0; Mismatches 799; Indels 9; Gaps 4;

QY 7 GGGGTTAGATCCTGCGGGGTTTATTTCATTCATTTGGCTTGAAGTCGTCAGGTCAGGG 66

Db 129 GGGGTCTCGGCGGGGGGCATTCTTTTCACGGCAAGGTGGTGAATTCGCGAGGTCACTC 188

QY 67 GAGTGTGCCCGAAAAACATTGAGAGGAAAAACAAACCCGATGTTGATTTGGGGGAATCGG 126

Db 189 CCGGCGCGCGGTAGAGAACGGAGCGAAAAACGGAAAGCAATACGTGGTTTTCCGGACTGG 248

QY 127 GGGTTACGATAGGACGCGAGTACTGCTATCACCTT--GGCGGTCTCTTTGTTGAAAG 184

Db 249 CCGTTACGATGTTCTGAAG-AGTGAATGCCATCACCCAACAGGCTGGTCTCTCGTCGAAAG 307

QY 185 GAATAATTACTCTAGTGTGCACTCACATCTTCAACGCTTCCAGCACTTCAAAAAGATCT 244

Db 308 GAACAAAACTGTGGTTACAACA---ACACCTTCCAGCTGCCGGCTTCAAAAAGATCC 364

QY 245 TGGTAGCAAAACCGCGCGAAATCGCGTCCGTGCTTCCGTGCAAGCACTCGAAACCGGTG 304

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QY 725 GCGGTATGCGTTTGTGTTTTCACCTGATGAGCTTCGCAATTAGCAACAGACATCTC 784

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Db	3242	CGAAGCCGACCGAGGAGTTCCTTGAGCACCGTCGCCGCTTCGGCAACACCTCCGCCCTGG	3301
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Db	3302	ATGACCGCGAGTTCTTCTACGGCTTGAAGGAGGACGTGAGGAGTGATCCGACTGACCG	3361
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Db	3362	GTGTGTCCACCCCGATGGTGGTCCGCCCTGGATGCGGTGTCCGAACCGGATGACAAAGGCA	3421
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Search completed: March 24, 2004, 00:13:39
Job time : 13746 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 17:20:33 ; Search time 1295 Seconds
(without alignments)
11878.552 Million cell updates/sec

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Perfect score: 3621
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s:*
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9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3621	100.0	3621	5	AAF32165 Coryneb
3	3621	100.0	3621	6	AAD42046 Coryneb
4	3621	100.0	3621	8	ACA62133 DNA encod
5	3621	100.0	349980	5	AAB68526 C glutami
6	3576.4	98.8	3728	2	AAX24102 C. glutam
7	3420	94.4	3420	5	AAH65730 C glutami
8	3398.8	93.9	3474	6	ABK52832 Coryneb
9	2279.6	63.0	4013	5	AAF87437 Coryneb
10	1927.4	53.2	3423	7	ACA29831 Prokaryot
11	1708	47.2	1719	4	AAF71419 Coryneb
12	1395	38.5	1406	4	AAF71420 Coryneb
13	1361.6	37.6	3381	7	ACA37896 Prokaryot
14	1294.4	35.7	3384	7	ACA40756 Prokaryot
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16	1294.4	35.7	110000	4	Continuation (34 o
17	1292.2	35.7	3381	7	ACA38630 Prokaryot
18	1249.6	34.5	32155	9	ADB74252 Mycobacte
19	1033	28.5	1083	4	AAF71418 Coryneb
20	1033	28.5	1083	4	AAF71417 Coryneb
21	907	25.0	939	4	AAF71415 Coryneb
22	907	25.0	939	4	AAF71416 Coryneb
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24	681	18.8	3945	7	ABT41829 Toxicity
25	681	18.8	3945	9	ADB59092 Toxicity
26	681	18.8	3945	9	ADB52590 Primary r
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28	668.4	18.5	4138	4	ABL19577 Drosophil
29	668.4	18.5	4308	4	ABL19575 Drosophil
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ALIGNMENTS

RESULT 1
AAA47533
ID AAA47533 standard; DNA; 3621 BP.
XX
AC AAA47533;
XX
DT 20-OCT-2000 (first entry)
XX
DE Sequence encoding pyruvate carboxylase of C. glutamicum.
XX
KW Pyruvate carboxylase; expression; amino acid biosynthesis; lysine;
KW glutamic acid; oxaloacetate; fermentation; biosynthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
FH Key Location/Qualifiers
FT CDS 199
FT /*tag= a
FT /product= "Pyruvate carboxylase"
FT /transl_except= (pos:199..202, aa:Met)
XX
PN WO200039305-A1.
XX
PD 06-JUL-2000.
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PF 23-DEC-1998; 98WO-US027301.
XX
PR 23-DEC-1998; 98WO-US027301.
XX
PA (SINS/) SINSKEY A J.
PA (LESS/) LESSARD P A.
PA (WILL/) WILLIS L B.
XX
PI Sinskey AJ, Lessard PA, Willis LB;
XX
DR WPI; 2000-465746/40.
DR P-PSDB; AAB01436.
XX
PT Novel polynucleotides encoding Corynebacterium glutamicum pyruvate
PT carboxylase useful for industrial fermentation processes comprises a
PT specific nucleotide sequence.
XX
PS Claim 3; Fig 1; Sipp; English.
XX
CC The pyruvate carboxylase of Corynebacterium glutamicum can be used for
CC producing amino acids, preferably lysine and glutamic acid in industrial

CC fermentations and for replenishing oxaloacetate consumed for biosynthesis
CC during growth. By incorporating the pyruvate carboxylase gene in
CC expression vectors levels of expression can be 2 - 20 fold higher than in
CC Corynebacterium glutamicum
XX
SQ Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;

Query Match 100.0%; Score 3621; DB 3; Length 3621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1021 TCCATTTGGTTACCAAGGCGGGAAACCGTGGAAATTTTGGTCGATGAAAAAGGCAACCAC 1080
QY 1081 GTCTTTCATCGAAATGAACCCACGATATCCAGGTTGAGCACACCGTGAAGAAAGTCACC 1140
DB 1081 GTCTTTCATCGAAATGAACCCACGATATCCAGGTTGAGCACACCGTGAAGAAAGTCACC 1140
QY 1141 GAGGTGGACCTGTTGAAGGCGCAGATGCGCTTGGCTGCTGTCGCAACCTTGAAGAAATTG 1200
DB 1141 GAGGTGGACCTGTTGAAGGCGCAGATGCGCTTGGCTGCTGTCGCAACCTTGAAGAAATTG 1200
QY 1201 GGTCTGACCCAAAGATAAGATCAAGACCCACCGTGCAGCACTGAGTGGCGCATCACCAAG 1260
DB 1201 GGTCTGACCCAAAGATAAGATCAAGACCCACCGTGCAGCACTGAGTGGCGCATCACCAAG 1260
QY 1261 GAAAGATCCAAACAAACCGCTTCCGCCAGATACCGGAACTATCAACCGGTACCGCTCACCA 1320
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QY 1321 GCGGAGCTGGCGTTCGTCTTGACCGGTGAGTCAAGCTGAGTGGGGAATCAACCGCACAC 1380
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QY 1741 CGCTGAAGCAGCTTGGCCAGCCGCTTGGCTGCTGATCTCCGTGAGCAGGACGACTG 1800
DB 1741 CGCTGAAGCAGCTTGGCCAGCCGCTTGGCTGCTGATCTCCGTGAGCAGGACGACTG 1800
QY 1801 GCAGTTACTGATACCACTTCCGCGATGCACACCAAGCTCTTTGCTTGGACCCGAGTCCGC 1860
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QY 1861 TCATTGCACTGAAGCCTGCGGAGGCGCGCTGCAAGCTGACTCTCTGAGCTTTTGTCC 1920
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3241 CCAGATGTGGCCACCCCACTGTTGTTGCTGAGTGCATCTCTGAGCCAGACGATAAG 3300
Db |||||
3241 CCAGATGTGGCCACCCCACTGTTGTTGCTGAGTGCATCTCTGAGCCAGACGATAAG 3300
Qy |||||
3301 GGTATGCGCAATGTTGTGGCCAACTGTTGCTGAGTGCATCTCTGAGCCAGTCCGCGTGC 3360
Db |||||
3301 GGTATGCGCAATGTTGTGGCCAACTGTTGCTGAGTGCATCTCTGAGCCAGTCCGCGTGC 3360
Qy |||||
3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGAGATTCCTCCAACAAAGGCCAT 3420
Db |||||
3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGAGATTCCTCCAACAAAGGCCAT 3420
Qy |||||
3421 GTTGTGCAACCAATCGTGGTGTGTCACCGTGAATGTTGCTGAAGGTGATGAGTCAAG 3480
Db |||||
3421 GTTGTGCAACCAATCGTGGTGTGTCACCGTGAATGTTGCTGAAGGTGATGAGTCAAG 3480
Qy |||||
3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
Db |||||
3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
Qy |||||
3541 GTTGACGGCAAAATCGATCGCGTGTGTTGCTGCTGCTCAACGAAGGTGGAAGGTGGCGAC 3600
Db |||||
3541 GTTGACGGCAAAATCGATCGCGTGTGTTGCTGCTGCTGCTCAACGAAGGTGGAAGGTGGCGAC 3600
Qy |||||
3601 TTGATCGTCTGCTGTTTCTTAA 3621
Db |||||
3601 TTGATCGTCTGCTGTTTCTTAA 3621

RESULT 2

AAF32165
ID AAF32165 standard; DNA; 3621 BP.

XX AAF32165;

XX 12-APR-2001 (first entry)

XX Corynebacterium glutamicum pyruvate carboxylase coding sequence.

XX Pyruvate carboxylase; anaplerotic pathway; industrial fermentation;
KW oxaloacetate; ds.

XX Corynebacterium glutamicum.

XX US6171833-B1.

XX 09-JAN-2001.

XX 23-DEC-1998; 98US-00220081.

XX 23-DEC-1998; 98US-00220081.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Sinskey AJ, Lessard PA, Willis LB;

XX WPI; 2001-122330/13.

XX P-PSDB; AAB57129.

XX Novel nucleic acid encoding pyruvate carboxylase from Corynebacterium
PT glutamicum, for replenishing oxaloacetate consumed during lysine and
PT glutamic acid production in industrial fermentations.

XX Claim 2; Col 23-30; 29pp; English.

XX

CC The present invention provides the protein and coding sequences of the
CC Corynebacterium glutamicum pyruvate carboxylase protein. This is an
CC enzyme in the anaplerotic pathway. It can be used in the replenishment of
CC oxaloacetate consumed during lysine and glutamic acid production in
CC industrial fermentation
XX
SQ Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;
Query Match 100.0%; Score 3621; DB 5; Length 3621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGGGGCGGGTTAGATCCTGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
Db 1 TGGGGCGGGTTAGATCCTGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
QY 61 TCAGGGGAGTGTGCCCCGAAACATTGAGAGGAAACAAAAACCGATGTTTGAATTGGGG 120
Db 61 TCAGGGGAGTGTGCCCCGAAACATTGAGAGGAAACAAAAACCGATGTTTGAATTGGGG 120
QY 121 AATCGGGGTTACGATACTAGACCGCAGTGACTGCTATCACCCCTTGGCGGCTCTTTGTTG 180
Db 121 AATCGGGGTTACGATACTAGACCGCAGTGACTGCTATCACCCCTTGGCGGCTCTTTGTTG 180
QY 181 AAAGGAATAATTACTCTAGTGTGCACTCACACATCTTCAACGCTTCCAGCAFTCAAAAAG 240
Db 181 AAAGGAATAATTACTCTAGTGTGCACTCACACATCTTCAACGCTTCCAGCAFTCAAAAAG 240
QY 241 ATCTTGTGAGCAAAACCGCGGGAATCGCGGTCCGTTCCGTGCGAGCACTCGAAACC 300
Db 241 ATCTTGTGAGCAAAACCGCGGGAATCGCGGTCCGTTCCGTGCGAGCACTCGAAACC 300
QY 301 GGTGACGACCGGTAGCTATTTACCCCGTGAAGATCGGGGATCATTTCCACCGCTCTTTT 360
Db 301 GGTGACGACCGGTAGCTATTTACCCCGTGAAGATCGGGGATCATTTCCACCGCTCTTTT 360
QY 361 GCTTCTGAAGCTGTCCGATTTGTTACCGGAGCTCACAGTCAAGGCGTACCTGGACATC 420
Db 361 GCTTCTGAAGCTGTCCGATTTGTTACCGGAGCTCACAGTCAAGGCGTACCTGGACATC 420
QY 421 GATGAAATATCGGTGTCAGCTAAAGGTTAAAGCAGATGCGCATTTACCCGGGATACGGC 480
Db 421 GATGAAATATCGGTGTCAGCTAAAGGTTAAAGCAGATGCGCATTTACCCGGGATACGGC 480
QY 481 TTCTGTCTGAAATGCCCCAGCTTGGCCGCGAGTGTGCGGAAACCGCATTTACTTTTATT 540
Db 481 TTCTGTCTGAAATGCCCCAGCTTGGCCGCGAGTGTGCGGAAACCGCATTTACTTTTATT 540
QY 541 GGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGGTAACCGCGCG 600
Db 541 GGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGGTAACCGCGCG 600
QY 601 AAGAAGGCTGGTCTGCCAGTTTGGCGGAATCCACCCGAGCAAAAACATCGATGAGATC 660
Db 601 AAGAAGGCTGGTCTGCCAGTTTGGCGGAATCCACCCGAGCAAAAACATCGATGAGATC 660
QY 661 GTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGTTGGTGC 720
Db 661 GTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGTTGGTGC 720
QY 721 GGACGCGGTATGCGTTTGTGTTTCACTGATGAGCTTCGCAAAATTAGCAACAGAAGCA 780
Db 721 GGACGCGGTATGCGTTTGTGTTTCACTGATGAGCTTCGCAAAATTAGCAACAGAAGCA 780
QY 781 TCTCGTGAAGCTGAAGCGGCTTTCGCGGATGGCGGATATGTGCAACGCTGTGATT 840
Db 781 TCTCGTGAAGCTGAAGCGGCTTTCGCGGATGGCGGATATGTGCAACGCTGTGATT 840
QY 841 AACCCCTCAGCATATTGAAGTGCAGATCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
Db 841 AACCCCTCAGCATATTGAAGTGCAGATCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
QY 901 TATGAACGCTGACTGCTCACTGCAGCGTCTGTCACCAAAAAGTTGTGAAATTGCGCCAGCA 960

Db 901 TATGAACGCTGACTGCTCACTGCAGCGTCGTACCAAAAAAGTTGTGAAATTGCGCCAGCA 960
QY 961 CAGCATTGGATCCAGAACTCGTGTATCGCAATTTGTGCGGATGCAAGTAAGTTCTGCCGC 1020
Db 961 CAGCATTGGATCCAGAACTCGTGTATCGCAATTTGTGCGGATGCAAGTAAGTTCTGCCGC 1020
QY 1021 TCCATTGGTTACAGGGCGCGGAAACCGTGGAAATCTTGGTCGATGAAAAAGGCAACAC 1080
Db 1021 TCCATTGGTTACAGGGCGCGGAAACCGTGGAAATCTTGGTCGATGAAAAAGGCAACAC 1080
QY 1081 GTCTTCATCGAAATGAACCCACGATATCCAGGTTGAGCACACCGTGTGAAGAAAGTCACC 1140
Db 1081 GTCTTCATCGAAATGAACCCACGATATCCAGGTTGAGCACACCGTGTGAAGAAAGTCACC 1140
QY 1141 GAGTGGACCTGGTGAAGCGCGAGATGCGCTTGGCTGTGGTCAACCTTGAAGGAATTG 1200
Db 1141 GAGTGGACCTGGTGAAGCGCGAGATGCGCTTGGCTGTGGTCAACCTTGAAGGAATTG 1200
QY 1201 GGTCTGACCCAAAGATAAGATCAAGACCCACCGTGCAGCACTGCAGTCCGCAATCACCACG 1260
Db 1201 GGTCTGACCCAAAGATAAGATCAAGACCCACCGTGCAGCACTGCAGTCCGCAATCACCACG 1260
QY 1261 GAAGATCCAAACAAACGGCTTCCGCCAGATACCGGAACTATCACCGCTACCGTCAACA 1320
Db 1261 GAAGATCCAAACAAACGGCTTCCGCCAGATACCGGAACTATCACCGCTACCGTCAACA 1320
QY 1321 GCGGAGCTGGCGTTCTGCTTACCGGTGCAGCTCAGCTCGTGGGGAATCACCGCACAC 1380
Db 1321 GCGGAGCTGGCGTTCTGCTTACCGGTGCAGCTCAGCTCGTGGGGAATCACCGCACAC 1380
QY 1381 TTTGACTCCATGCTGGTGAATGACCTGCGGTGCTCCGACTTTTGAACCTGCTGTTGCT 1440
Db 1381 TTTGACTCCATGCTGGTGAATGACCTGCGGTGCTCCGACTTTTGAACCTGCTGTTGCT 1440
QY 1441 CGTGACAGCGCGCTTGGCTGAGTTCAACCGTGTCTGCTGTTGCAACCAACATTTGTTTC 1500
Db 1441 CGTGACAGCGCGCTTGGCTGAGTTCAACCGTGTCTGCTGTTGCAACCAACATTTGTTTC 1500
QY 1501 TTGCGTGGTGTCTGCGGGAAGAGGACTTCACTTCCAGCGCATCGCCACCGGATTCATT 1560
Db 1501 TTGCGTGGTGTCTGCGGGAAGAGGACTTCACTTCCAGCGCATCGCCACCGGATTCATT 1560
QY 1561 GCCGATCACCCCGCACCTCTTCAAGGCTCCACCTGCTGATGATGAGCAGGACGCACTCTG 1620
Db 1561 GCCGATCACCCCGCACCTCTTCAAGGCTCCACCTGCTGATGATGAGCAGGACGCACTCTG 1620
QY 1621 GATTACTTGGCAGATGTCAACCGTGAACAAGCCTCATGTTGCTGCTCCAAAGGATGTTGCA 1680
Db 1621 GATTACTTGGCAGATGTCAACCGTGAACAAGCCTCATGTTGCTGCTCCAAAGGATGTTGCA 1680
QY 1681 GCTCCTATCGATAAGCTGCTTAACATCAAGGATCTGCCACTGCCACGCGTTCCCGTGAC 1740
Db 1681 GCTCCTATCGATAAGCTGCTTAACATCAAGGATCTGCCACTGCCACGCGTTCCCGTGAC 1740
QY 1741 CGCCTGAAGCAGCTTGGCCAGCGCGGTTTGTCTGCTGATCTCCGTGAGCAGGACGCACTG 1800
Db 1741 CGCCTGAAGCAGCTTGGCCAGCGCGGTTTGTCTGCTGATCTCCGTGAGCAGGACGCACTG 1800
QY 1801 GCAGTTACTGATACCACTTCCGCGATGCACACAGTCTTGTGCTTGGACCCGAGTCCGC 1860
Db 1801 GCAGTTACTGATACCACTTCCGCGATGCACACAGTCTTGTGCTTGGACCCGAGTCCGC 1860
QY 1861 TCATTGCACTGAAGCCTGCGGAGAGGCGCTCGAAAGTGAAGTGAAGTCTTGTGTC 1920
Db 1861 TCATTGCACTGAAGCCTGCGGAGAGGCGCTCGAAAGTGAAGTGAAGTCTTGTGTC 1920
QY 1921 GTGAGGCTGGGCGCGGACCTACGATGTGGCGATGCGTTTCTCTTTGAGGATCCG 1980
Db 1921 GTGAGGCTGGGCGCGGACCTACGATGTGGCGATGCGTTTCTCTTTGAGGATCCG 1980
QY 1981 TGGGACAGGCTCGACGAGCTGCGGAGGCGGATGCCGAAATGTAAACATTCAGATGCTGTT 2040

Db 1981 TGGGACAGGCTCGACGAGCTGCGCGAGGCGGATGCCGAATGTAAACATTTCAGATGCTGCTT 2040
Qy 2041 CGCGGCGCAACACCGTGGGATACACCCCGTACCAGACTCCGTCGTCGCCGCGGTTGTT 2100
Db 2041 CGCGGCGCAACACCGTGGGATACACCCCGTACCAGACTCCGTCGTCGCCGCGGTTGTT 2100
Qy 2101 AAGGAAGCTGCCAGCTCCGGCGTGGAGATCTTCCGCATCTTCGACCGCTTAAACAGCTC 2160
Db 2101 AAGGAAGCTGCCAGCTCCGGCGTGGAGATCTTCCGCATCTTCGACCGCTTAAACAGCTC 2160
Qy 2161 TCCAGATGGTCCAGCAATCGACGAGTCTTGAGACCAAACACCGCGGTAGCCGAGGTG 2220
Db 2161 TCCAGATGGTCCAGCAATCGACGAGTCTTGAGACCAAACACCGCGGTAGCCGAGGTG 2220
Qy 2221 GCTATGGCTTAACTTGGTGATCTCTCTGATCCAAATGAAAGCTTACACCCCTGGATTAC 2280
Db 2221 GCTATGGCTTAACTTGGTGATCTCTCTGATCCAAATGAAAGCTTACACCCCTGGATTAC 2280
Qy 2281 TACCTAAGATGGCAGAGGAGATCGTCAAGTCTGGCGTCAATCTTGGCCATTAAAGGAT 2340
Db 2281 TACCTAAGATGGCAGAGGAGATCGTCAAGTCTGGCGTCAATCTTGGCCATTAAAGGAT 2340
Qy 2341 ATGGCTGCTCTGCTTCCGCCAGCTGCGGTAAACCAAGCTGGTCAACCGCACTGCGCCGTGAA 2400
Db 2341 ATGGCTGCTCTGCTTCCGCCAGCTGCGGTAAACCAAGCTGGTCAACCGCACTGCGCCGTGAA 2400
Qy 2401 TTCGATCTGCCAGTGACGTCACACCCACGACACTGCGGTGCGCAGCTGGCAACCTTAC 2460
Db 2401 TTCGATCTGCCAGTGACGTCACACCCACGACACTGCGGTGCGCAGCTGGCAACCTTAC 2460
Qy 2461 TTTGCTGCAGCTCAAGCTGGTGAGATGCTGTGACGGTGCTTCCGACCACTGTCTGCG 2520
Db 2461 TTTGCTGCAGCTCAAGCTGGTGAGATGCTGTGACGGTGCTTCCGACCACTGTCTGCG 2520
Qy 2521 ACCACCTCCAGCATCCCTGTCTGCCATTGTTGCTGCATTCCGCGCACACCCGTCGCGAT 2580
Db 2521 ACCACCTCCAGCATCCCTGTCTGCCATTGTTGCTGCATTCCGCGCACACCCGTCGCGAT 2580
Qy 2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTAACCGGTGCGTCTACCGCCACGAA 2640
Db 2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTAACCGGTGCGTCTACCGCCACGAA 2640
Qy 2641 CTGTACCTGCCATTGAGTCTGGAAACCCAGGCCCAACCGGTGCGTCTACCGCCACGAA 2700
Db 2641 CTGTACCTGCCATTGAGTCTGGAAACCCAGGCCCAACCGGTGCGTCTACCGCCACGAA 2700
Qy 2701 ATCCCAGGGGACAGTTGTCCAAACCTGCGTGACAGGCCACCGCACTGGCCCTTGGCGAT 2760
Db 2701 ATCCCAGGGGACAGTTGTCCAAACCTGCGTGACAGGCCACCGCACTGGCCCTTGGCGAT 2760
Qy 2761 CGTTTCGAACCTCATCGAAGACAACTACGACGCGGTTAATGAGATGCTGGGACGCCCAACC 2820
Db 2761 CGTTTCGAACCTCATCGAAGACAACTACGACGCGGTTAATGAGATGCTGGGACGCCCAACC 2820
Qy 2821 AAGGTCACCCCATCCCTCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGGCGGT 2880
Db 2821 AAGGTCACCCCATCCCTCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGGCGGT 2880
Qy 2881 GTGGATCCAGCAGACTTGTCTGCCGATCCCAAAAGTACGACATCCAGACTCTGTCTATC 2940
Db 2881 GTGGATCCAGCAGACTTGTCTGCCGATCCCAAAAGTACGACATCCAGACTCTGTCTATC 2940
Qy 2941 GCGTTCTGCGCGGAGCTTGGTAACCCCTCAGGTGGCTGGCCAGAGCCACTGCGCAC 3000
Db 2941 GCGTTCTGCGCGGAGCTTGGTAACCCCTCAGGTGGCTGGCCAGAGCCACTGCGCAC 3000
Qy 3001 CGCGCACTGGAAGCGCTCCGAAGGCAAGCACTCTGACGGAAGTTCTTGAGGAAGAG 3060
Db 3001 CGCGCACTGGAAGCGCTCCGAAGGCAAGCACTCTGACGGAAGTTCTTGAGGAAGAG 3060
Qy 3061 CAGGCGCACCTCGACGCTGATGATTCGAAGGAACGTGCAATAGCCTCAACCGCCTGCTG 3120
Db 3061 CAGGCGCACCTCGACGCTGATGATTCGAAGGAACGTGCAATAGCCTCAACCGCCTGCTG 3120

Qy 3121 TTCCCGAAGCCCAACCGAAGATTCTCTCGAGCACCGTCGCGCTTCGGCAACACCTCTGCG 3180
Db 3121 TTCCCGAAGCCCAACCGAAGATTCTCTCGAGCACCGTCGCGCTTCGGCAACACCTCTGCG 3180
Qy 3181 CTGGATGATCGTGAATTCTTACGGCCTGGTCGAAAGCGCGAGACTTTGATCCGCCTG 3240
Db 3181 CTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAAGCGCGAGACTTTGATCCGCCTG 3240
Qy 3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
Db 3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
Qy 3301 GGATGCGCAATGTTGTGGCCAAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
Db 3301 GGATGCGCAATGTTGTGGCCAAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
Qy 3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGCGAGATTCTCCAACAAAGGCCAT 3420
Db 3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGCGAGATTCTCCAACAAAGGCCAT 3420
Qy 3421 GTTGTGCAACCATTCGCTGCTGTGTTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
Db 3421 GTTGTGCAACCATTCGCTGCTGTGTTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAG 3480
Qy 3481 GCTGGAGATGAGTGCATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
Db 3481 GCTGGAGATGAGTGCATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCT 3540
Qy 3541 GTTGACGGCAAAATCGATCGCGTTGCTGCTGCAACGAAGGTGGAAGTGGCGAC 3600
Db 3541 GTTGACGGCAAAATCGATCGCGTTGCTGCTGCAACGAAGGTGGAAGTGGCGAC 3600
Qy 3601 TTGATCGTCTGCTTTCCTAA 3621
Db 3601 TTGATCGTCTGCTTTCCTAA 3621

RESULT 3
AAD42046
ID AAD42046 standard; DNA; 3621 BP.
XX
AC AAD42046;
XX
DT 04-NOV-2002 (first entry)
XX
DE Corynebacterium glutamicum pyruvate carboxylase DNA.
XX
KW Pyruvate carboxylase; anaplerotic enzyme; industrial fermentation;
KW oxaloacetate; growth; enzyme; gene; ds..
XX
OS Corynebacterium glutamicum.
FH Key Location/Qualifiers
CDS 199..3621
FT /*tag= a
FT /product= "Pyruvate carboxylase protein"
FT /transl_except= (pos:199..201, aa:Met)
XX
US6403351-B1.
PN
PD 11-JUN-2002.
XX
PF 03-OCT-2000; 2000US-00677575.
XX
PR 23-DEC-1998; 98US-00220081.
XX
PA (ARCH) ARCHER-DANIELS MIDLAND CO.
XX
PI Sinskey AJ, Lessard PA, Willis LB;
XX
DR WPI; 2002-536037/57.
DR P-PSDB; AAE25601.

XX Novel pyruvate carboxylase polypeptide, useful for replenishing
PT oxaloacetate consumed for biosynthesis during growth, or lysine and
PT glutamic acid production in industrial fermentation.
XX
XX Disclosure; Col 23-30; 28pp; English.
XX
CC The present invention relates to novel pyruvate carboxylase proteins and
CC polynucleotides encoding such proteins. Sequences of the invention are
CC important anaplerotic enzymes for replenishing oxaloacetate consumed for
CC biosynthesis during growth, or lysine and glutamic acid production in
CC industrial fermentation. The present sequence is C. glutamicum pyruvate
CC carboxylase DNA
XX
SQ Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;
Query Match 100.0%; Score 3621; DB 6; Length 3621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGGGGCGGGTTAGATCCTGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGACG 60
Db 1 TGGGGCGGGTTAGATCCTGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGACG 60
QY 61 TCAGGGAGTGTGCCCCGAAACATTGAGAGGAAACAAACAAACCCGATGTTGATGGGG 120
Db 61 TCAGGGAGTGTGCCCCGAAACATTGAGAGGAAACAAACAAACCCGATGTTGATGGGG 120
QY 121 AATCGGGGTTACGATACCTAGGACGAGTACTGCTATCACCTTTGGCGGCTCTTTG 180
Db 121 AATCGGGGTTACGATACCTAGGACGAGTACTGCTATCACCTTTGGCGGCTCTTTG 180
QY 181 AAAGGAATAATTACTCTAGTGTGACTCACACATCTTCAACGCTTCCAGCATCAAAAAG 240
Db 181 AAAGGAATAATTACTCTAGTGTGACTCACACATCTTCAACGCTTCCAGCATCAAAAAG 240
QY 241 ATCTTGGTAGCAACCGCGGCGAAATCGCGTCCGTCCTTCCGTCAGCACTCGAAACC 300
Db 241 ATCTTGGTAGCAACCGCGGCGAAATCGCGTCCGTCCTTCCGTCAGCACTCGAAACC 300
QY 301 GGTGCAGCCAGGTAGCTATTACCCCGGTGAAGATCGGGGATCATTCACCGCTCTTT 360
Db 301 GGTGCAGCCAGGTAGCTATTACCCCGGTGAAGATCGGGGATCATTCACCGCTCTTT 360
QY 361 GCTTCTGAGCTGTCGGCATTTGGTACCGAAGGCTCACCAAGTCAAGGCTACCTGGACATC 420
Db 361 GCTTCTGAGCTGTCGGCATTTGGTACCGAAGGCTCACCAAGTCAAGGCTACCTGGACATC 420
QY 421 GATGAAATATCGGTGCAGCTAAAGAAAGTTAAAGCAGATGCCATTACCCGGGATACGGC 480
Db 421 GATGAAATATCGGTGCAGCTAAAGAAAGTTAAAGCAGATGCCATTACCCGGGATACGGC 480
QY 481 TTCCTGTCTGAAATGCCCCAGCTTGGCCGGAGTGTGCGGAAACCGCATTACTTTATT 540
Db 481 TTCCTGTCTGAAATGCCCCAGCTTGGCCGGAGTGTGCGGAAACCGCATTACTTTATT 540
QY 541 GGCCCCAACCCGAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAAACCGCGCG 600
Db 541 GGCCCCAACCCGAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAAACCGCGCG 600
QY 601 AAGAGGCTGGTCTGCCAGTTTGGCGGAATCCACCCCGAGCAAAACATCGATGAGATC 660
Db 601 AAGAGGCTGGTCTGCCAGTTTGGCGGAATCCACCCCGAGCAAAACATCGATGAGATC 660
QY 661 GTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGAGTTGCCGGTGGTGGC 720
Db 661 GTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGAGTTGCCGGTGGTGGC 720
QY 721 GGACGCGGTATGCGTTTGTGCTTCACTGTAGCTTCCGAAATTAGCAACAGAGCA 780
Db 721 GGACGCGGTATGCGTTTGTGCTTCACTGTAGCTTCCGAAATTAGCAACAGAGCA 780
QY 781 TCTCGTGAAGCTGAAGCGGCTTTTCGGCGATGGCGGGTATATGTGCAACGTGTGTGATT 840

Db 781 TCTCGTGAAGCTGAAGCGGCTTTTCGGCGATGGCGGGTATATGTGCAACGTGTGTGATT 840
QY 841 AACCCCTCAGCATATTGAAGTGCAGATCCTTTGGCGATCACACTGGAGAGTTGTACACCTT 900
Db 841 AACCCCTCAGCATATTGAAGTGCAGATCCTTTGGCGATCACACTGGAGAGTTGTACACCTT 900
QY 901 TATGAACGTGACTGCTCACTGCAGCGTGCACCAAAAAAGTTGTGCAAAATTCGCCAGCA 960
Db 901 TATGAACGTGACTGCTCACTGCAGCGTGCACCAAAAAAGTTGTGCAAAATTCGCCAGCA 960
QY 961 CAGCATTTGGATCCAGAACTGCGTGTATCGCAATTTGTGCGGATGCAAGTAAGTTCTGCCGC 1020
Db 961 CAGCATTTGGATCCAGAACTGCGTGTATCGCAATTTGTGCGGATGCAAGTAAGTTCTGCCGC 1020
QY 1021 TCCATTGGTTACCAGGCGCGGGAACCCGTGGAATTTTGGTTCGATGAAAAAGGGCAACCAC 1080
Db 1021 TCCATTGGTTACCAGGCGCGGGAACCCGTGGAATTTTGGTTCGATGAAAAAGGGCAACCAC 1080
QY 1081 GTCTTTCATCGAAATGAACCCACGATCCAGGTTGAGCACACCCGTGACTGAAGAAAGTCACC 1140
Db 1081 GTCTTTCATCGAAATGAACCCACGATCCAGGTTGAGCACACCCGTGACTGAAGAAAGTCACC 1140
QY 1141 GAGTGGACCTGGTGAAGCGCAGATGCGCTTGGCTGCTGGTCAACCTTGAAGGAATTG 1200
Db 1141 GAGTGGACCTGGTGAAGCGCAGATGCGCTTGGCTGCTGGTCAACCTTGAAGGAATTG 1200
QY 1201 GGTCTGACCCCAAGATAAGATCAAGACCCACCGTGCAGCACTGCAGTCCCGCATCACCAAG 1260
Db 1201 GGTCTGACCCCAAGATAAGATCAAGACCCACCGTGCAGCACTGCAGTCCCGCATCACCAAG 1260
QY 1261 GAAGATCCAAACAACCGGCTTCCGCCCCAGATACCGGAACATATCACCGCTACCGCTCACCA 1320
Db 1261 GAAGATCCAAACAACCGGCTTCCGCCCCAGATACCGGAACATATCACCGCTACCGCTCACCA 1320
QY 1321 GCGGAGCTGGCTTCTGTTGACGGTGCAGCTGCGTGGTGGCGAAATCACCGCACAC 1380
Db 1321 GCGGAGCTGGCTTCTGTTGACGGTGCAGCTGCGTGGTGGCGAAATCACCGCACAC 1380
QY 1381 TTTGACTCCATGCTGGTGAATAATGACCTGCGCTGGTTCGACTTTGAAACTGCTGTGCT 1440
Db 1381 TTTGACTCCATGCTGGTGAATAATGACCTGCGCTGGTTCGACTTTGAAACTGCTGTGCT 1440
QY 1441 CGTGACAGCGCGGCTTGGCTGAGTTTCAACCGTGTCTGGTGTGCAACCAACATTGGTTTC 1500
Db 1441 CGTGACAGCGCGGCTTGGCTGAGTTTCAACCGTGTCTGGTGTGCAACCAACATTGGTTTC 1500
QY 1501 TTGCGTGGCTTGTGCGGGAGAGGACTTCACTTCCAGCGCATCGCCACCGGATTCAAT 1560
Db 1501 TTGCGTGGCTTGTGCGGGAGAGGACTTCACTTCCAGCGCATCGCCACCGGATTCAAT 1560
QY 1561 GCGGATCACCCGACCTCTTTCAGGCTCCACCTGCTGATGATGAGCAGGACGATCCTG 1620
Db 1561 GCGGATCACCCGACCTCTTTCAGGCTCCACCTGCTGATGATGAGCAGGACGATCCTG 1620
QY 1621 GATTACTTGGCAGATGTCAACCGTGAACAAGCCTCATGGTGGCTCCAAAGGATGTTGCA 1680
Db 1621 GATTACTTGGCAGATGTCAACCGTGAACAAGCCTCATGGTGGCTCCAAAGGATGTTGCA 1680
QY 1681 GCTCCTATCGATAAGCTGCCATAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 1740
Db 1681 GCTCCTATCGATAAGCTGCCATAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 1740
QY 1741 CGCCTGAAGCAGCTTGGCCAGCCGCTTTGCTCGTATCTCCGTGAGCAGGACGCACTG 1800
Db 1741 CGCCTGAAGCAGCTTGGCCAGCCGCTTTGCTCGTATCTCCGTGAGCAGGACGCACTG 1800
QY 1801 GCAGTTACTGATACCACTTCCGCGATGCAACCAAGTCTTTGCTGCGACCCGAGTCCGC 1860
Db 1801 GCAGTTACTGATACCACTTCCGCGATGCAACCAAGTCTTTGCTGCGACCCGAGTCCGC 1860
QY 1861 TCATTGCACTGAAGCCTGCGGCGAGGCGCTGCAAAAGTCACTCCTGAGCTTTTGTCTC 1920

Db 1861 TCATTGCACTGAAGCCCTGCGGCAGAGGCCGTGCGAAAGCTGACTCCTGAGCTTTTGTCC 1920
QY 1921 GTGGAGGCTGGGGCGGCGACCTACGATGTGGCGATGCGTTTCTCTTTGAGGATCCG 1980
Db 1921 GTGGAGGCTGGGGCGGCGACCTACGATGTGGCGATGCGTTTCTCTTTGAGGATCCG 1980
QY 1981 TGGGACAGGCTGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTTCAGATGCTGCTT 2040
Db 1981 TGGGACAGGCTGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTTCAGATGCTGCTT 2040
QY 2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGCTCGCGCGCTTTGTT 2100
Db 2041 CGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGCTCGCGCGCTTTGTT 2100
QY 2101 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCACTCTTCGACGCGCTTAAACGACGTC 2160
Db 2101 AAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCACTCTTCGACGCGCTTAAACGACGTC 2160
QY 2161 TCCAGATGCGTCCAGCAATCGACGAGTCTCTGATCCAAATGAAAAGCTCTACACCTGGATTAC 2220
Db 2161 TCCAGATGCGTCCAGCAATCGACGAGTCTCTGATCCAAATGAAAAGCTCTACACCTGGATTAC 2220
QY 2221 GCTATGGCTTATTCTGGTATCTCTGATCCAAATGAAAAGCTCTACACCTGGATTAC 2280
Db 2221 GCTATGGCTTATTCTGGTATCTCTGATCCAAATGAAAAGCTCTACACCTGGATTAC 2280
QY 2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAAGGAT 2340
Db 2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAAGGAT 2340
QY 2341 ATGGCTGGTCTGCTTCGCCAGCTGCGGTAAACCAAGCTGGTCAACCGCACTGCGCCGTGAA 2400
Db 2341 ATGGCTGGTCTGCTTCGCCAGCTGCGGTAAACCAAGCTGGTCAACCGCACTGCGCCGTGAA 2400
QY 2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGTGGCCAGCTGGCAACCTAC 2460
Db 2401 TTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGTGGCCAGCTGGCAACCTAC 2460
QY 2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCGCGACCACTGTCTGGC 2520
Db 2461 TTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCGCGACCACTGTCTGGC 2520
QY 2521 ACCACTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCGCTGCGGAT 2580
Db 2521 ACCACTCCCAGCCATCCCTGTCTGCCATTGTTGCTGCATTCGCGCACACCGCTGCGGAT 2580
QY 2581 ACCGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGCGGAGCAGTGGCGGA 2640
Db 2581 ACCGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGCGGAGCAGTGGCGGA 2640
QY 2641 CTGTACTGCCATTGAGTCTGGAACCCCGAGCCCAACCGGTGCGGTCTACCGCCACGAA 2700
Db 2641 CTGTACTGCCATTGAGTCTGGAACCCCGAGCCCAACCGGTGCGGTCTACCGCCACGAA 2700
QY 2701 ATCCAGGCGGACAGTTGTCCAACTGCGTGCAAGGCGGACCTGCGGTGCGGTCTACCGCCACGAA 2760
Db 2701 ATCCAGGCGGACAGTTGTCCAACTGCGTGCAAGGCGGACCTGCGGTGCGGTCTACCGCCACGAA 2760
QY 2761 CGTTTCGAACCTCATCGAAGCAACTACGCGAGCCGTTAATGAGATGCTGGGACGCGCCAAAC 2820
Db 2761 CGTTTCGAACCTCATCGAAGCAACTACGCGAGCCGTTAATGAGATGCTGGGACGCGCCAAAC 2820
QY 2821 AAGGTACCCCATCTCCAAAGTTGTGGCGACCTCGCACTCCACCTCGTTGGTGGGGT 2880
Db 2821 AAGGTACCCCATCTCCAAAGTTGTGGCGACCTCGCACTCCACCTCGTTGGTGGGGT 2880
QY 2881 GTGGATCCAGCAGACTTTGTGCGCGATCCCAAAAGTACGACATCCAGACTCTGTCTATC 2940
Db 2881 GTGGATCCAGCAGACTTTGTGCGCGATCCCAAAAGTACGACATCCAGACTCTGTCTATC 2940
QY 2941 GCGTTCTCGCGGCGAGCTTGGTAAACCTCCAGGTGGTGGCGAGCCACTGCGGCACC 3000
Db 2941 GCGTTCTCGCGGCGAGCTTGGTAAACCTCCAGGTGGTGGCGAGCCACTGCGGCACC 3000

QY 3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCTCTGAGGAAGAG 3060
Db 3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCTCTGAGGAAGAG 3060
QY 3061 CAGGCGCACTCGACGCTGATGATTCGAAGGAACGTGCGCAATAGCCTCAACCGCCTGCTG 3120
Db 3061 CAGGCGCACTCGACGCTGATGATTCGAAGGAACGTGCGCAATAGCCTCAACCGCCTGCTG 3120
QY 3121 TTCCCGAAGCCAAACCGAAGAGTTCTCTGAGCAACCGTCCGCGCTTCGGCAACACCTCTGCG 3180
Db 3121 TTCCCGAAGCCAAACCGAAGAGTTCTCTGAGCAACCGTCCGCGCTTCGGCAACACCTCTGCG 3180
QY 3181 CTGGATGATCGTGAATTTCTTCTACGGCTGGTTCGAAGGCGCGGAGACTTTGATCCGCGCTG 3240
Db 3181 CTGGATGATCGTGAATTTCTTCTACGGCTGGTTCGAAGGCGCGGAGACTTTGATCCGCGCTG 3240
QY 3241 CCAGATGTGCGCAACCCCACTGCTGTTGCTGCGCTGGATCCGATCTCTGAGCCAGACGATAAG 3300
Db 3241 CCAGATGTGCGCAACCCCACTGCTGTTGCTGCGCTGGATCCGATCTCTGAGCCAGACGATAAG 3300
QY 3301 GGTATGCGCAATGTTGTGGCCCAACGTCAACGGCCAGATCCGCGCAATGCGTGTGCGTGAC 3360
Db 3301 GGTATGCGCAATGTTGTGGCCCAACGTCAACGGCCAGATCCGCGCAATGCGTGTGCGTGAC 3360
QY 3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAAGGAGGAGATTCTCTCAACCAAGGGCCAT 3420
Db 3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAAGGAGGAGATTCTCTCAACCAAGGGCCAT 3420
QY 3421 GTTGTGCACCAATTCGCTGGTGTGTCAACCGTGAATGGAAGCAACATCACTGCTTCT 3480
Db 3421 GTTGTGCACCAATTCGCTGGTGTGTCAACCGTGAATGGAAGCAACATCACTGCTTCT 3480
QY 3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACATCACTGCTTCT 3540
Db 3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACATCACTGCTTCT 3540
QY 3541 GTTGACGGCAAAATCGATCGCGTGTGTTCTCTGCTGCAACGAAGTGGAAGTGGCGGAC 3600
Db 3541 GTTGACGGCAAAATCGATCGCGTGTGTTCTCTGCTGCAACGAAGTGGAAGTGGCGGAC 3600
QY 3601 TTGATCGTCTGCTTTCTCTAA 3621
Db 3601 TTGATCGTCTGCTTTCTCTAA 3621

RESULT 4
ACA62133
ID ACA62133 standard; DNA; 3621 BP.
XX
AC ACA62133;
XX 25-AUG-2003 (first entry)
DT
XX DNA encoding Corynebacterium glutamicum pyruvate carboxylase.
DE
XX Pyruvate carboxylase; gene; anaplerotic enzyme; oxaloacetate;
KW biosynthesis; growth; lysine production; glutamic acid production;
KW industrial fermentation; gene; ds.
OS Corynebacterium glutamicum.
XX
FH Key Location/Qualifiers
CDS 199..3621
FT /*tag= a
FT /product= "Pyruvate carboxylase"
XX US2003027305-A1.
PN
XX 06-FEB-2003.
PD
XX 15-JAN-2002; 2002US-00045072.
PF
XX

PR 23-DEC-1998; 98US-00220081.
PR 03-OCT-2000; 2000US-00677575.
XX
XX
PA (ARCH) ARCHER-DANIELS MIDLAND CO.
PI Sinskey AJ, Lessard PA, Willis LB;
XX
XX WPI; 2003-479542/58.
DR P-PSDB; ABU10426.
XX
XX New pyruvate carboxylase from Corynebacterium glutamicum, useful as an
PT anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis
PT during growth, or for lysine or glutamic acid production in industrial
PT fermentations.
XX
PS Claim 2; Page 12-16; 29pp; English.
XX The invention describes a new isolated pyruvate carboxylase polypeptide
CC having an amino acid sequence at least 95% identical to a sequence
CC comprising 1140 amino acids from Corynebacterium glutamicum, or the
CC complete amino acid sequence encoded by the cosmid clone deposited with
CC the American Type Culture Collection. The polypeptide is useful as an
CC anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis
CC during growth. The polypeptide is also useful for lysine or glutamic acid
CC production in industrial fermentations. This sequence encodes
CC Corynebacterium glutamicum pyruvate carboxylase
XX
SQ Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;
Query Match 100.0%; Score 3621; DB 8; Length 3621;
Best local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGGGGCGGGGTAGATCCTGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
Db 1 TGGGGCGGGGTAGATCCTGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
QY 61 TCAGGGGAGTGTGCCGGAACATTGAGAGGAAACAAAAACCGATGTTTGATGGGGG 120
Db 61 TCAGGGGAGTGTGCCGGAACATTGAGAGGAAACAAAAACCGATGTTTGATGGGGG 120
QY 121 AATCGGGGTACGATAGGACGAGTGACTGCTATCACTCCCTTGGCGGTCTCTTTG 180
Db 121 AATCGGGGTACGATAGGACGAGTGACTGCTATCACTCCCTTGGCGGTCTCTTTG 180
QY 181 AAAGGAATAATTACTCTAGTGTGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
Db 181 AAAGGAATAATTACTCTAGTGTGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
QY 241 ATCTTGTAGCAACCGCGGGAATCGCGTCCGTGCTTCCGTGCAGCACTCGAAACC 300
Db 241 ATCTTGTAGCAACCGCGGGAATCGCGTCCGTGCTTCCGTGCAGCACTCGAAACC 300
QY 301 GGTGCAGCCACGGTAGCTATTTACCCCGTGAAGATCGGGGATCATTTCCACCGCTCTTT 360
Db 301 GGTGCAGCCACGGTAGCTATTTACCCCGTGAAGATCGGGGATCATTTCCACCGCTCTTT 360
QY 361 GCTTCTGAAGCTGTCCGCATTGTGTACCGAAGGCTCACCAAGTCAAGGCGTACCTGGACATC 420
Db 361 GCTTCTGAAGCTGTCCGCATTGTGTACCGAAGGCTCACCAAGTCAAGGCGTACCTGGACATC 420
QY 421 GATGAATAATTATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTACCCGGGATACGGC 480
Db 421 GATGAATAATTATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTACCCGGGATACGGC 480
QY 481 TTCTGTCTGAAATGCCCCAGCTTCCCCGGAGTGTGCGGAAACCGCATTACTTTATT 540
Db 481 TTCTGTCTGAAATGCCCCAGCTTCCCCGGAGTGTGCGGAAACCGCATTACTTTATT 540
QY 541 GGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGGGTAACCGCCGG 600
Db 541 GGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGGGTAACCGCCGG 600

QY 601 AAGAAGCGTGGTCTGCCAGTTTGGCGGAATCCACCCGAGCAAAACATCGATGAGATC 660
Db 601 AAGAAGCGTGGTCTGCCAGTTTGGCGGAATCCACCCGAGCAAAACATCGATGAGATC 660
QY 661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGTGGTGGC 720
Db 661 GTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGTGGTGGC 720
QY 721 GGACCGGTATGCGTTTGTGCTTCACTGATGAGCTTCGCAATTAGCAACAGAAGCA 780
Db 721 GGACCGGTATGCGTTTGTGCTTCACTGATGAGCTTCGCAATTAGCAACAGAAGCA 780
QY 781 TCTCGTGAAGCTGAAGCGGCTTTCCGCGATGGCGGCTATATGTCGAACGTGCTGTGATT 840
Db 781 TCTCGTGAAGCTGAAGCGGCTTTCCGCGATGGCGGCTATATGTCGAACGTGCTGTGATT 840
QY 841 AACCTCAGCATATTGAAGTCAGATCCTTGGCGGATCACACTGGAGAAGTTGTACACCTT 900
Db 841 AACCTCAGCATATTGAAGTCAGATCCTTGGCGGATCACACTGGAGAAGTTGTACACCTT 900
QY 901 TATGAACGTGACTGCTCACTGCAGCGTCTGTCACCAAAAAAGTTGTCGAAATTCGCCAGCA 960
Db 901 TATGAACGTGACTGCTCACTGCAGCGTCTGTCACCAAAAAAGTTGTCGAAATTCGCCAGCA 960
QY 961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
Db 961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
QY 1021 TCCATTGGTTACAGGGCGGGGAACCGTGGAAATTTCTGGTCGATGAAAAAGGGCAACCAC 1080
Db 1021 TCCATTGGTTACAGGGCGGGGAACCGTGGAAATTTCTGGTCGATGAAAAAGGGCAACCAC 1080
QY 1081 GTCTTCATCGAAATGAACCCACGTTATCCAGTTGAGCACACCGTGACTGAAGAAGTCACC 1140
Db 1081 GTCTTCATCGAAATGAACCCACGTTATCCAGTTGAGCACACCGTGACTGAAGAAGTCACC 1140
QY 1141 GAGTGCACCTGGTGAAGCGCGAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200
Db 1141 GAGTGCACCTGGTGAAGCGCGAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200
QY 1201 GGTCTGACCCAAGATAAGATCAAGACCCACCGTGACGACTGCGGCTACCCACG 1260
Db 1201 GGTCTGACCCAAGATAAGATCAAGACCCACCGTGACGACTGCGGCTACCCACG 1260
QY 1261 GAAGATCCAAACAAACCGCTTCCGCCCCAGATAACCGGAACTATCACCGCTACCCACCA 1320
Db 1261 GAAGATCCAAACAAACCGCTTCCGCCCCAGATAACCGGAACTATCACCGCTACCCACCA 1320
QY 1321 GGCGGAGCTGGCTTGGTGAAGCGGTGAGTCAAGTCCGCTGGTGGCGGAAATCACCGCACAC 1380
Db 1321 GGCGGAGCTGGCTTGGTGAAGCGGTGAGTCAAGTCCGCTGGTGGCGGAAATCACCGCACAC 1380
QY 1381 TTTGACTCCATGCTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1440
Db 1381 TTTGACTCCATGCTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1440
QY 1441 CGTGACAGCGCGCTTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1500
Db 1441 CGTGACAGCGCGCTTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1500
QY 1501 TTGCGTGGTGTGTCGCGGGAAGAGGACTTCACTTCCAGCGCATCGCCACCGGATTCATT 1560
Db 1501 TTGCGTGGTGTGTCGCGGGAAGAGGACTTCACTTCCAGCGCATCGCCACCGGATTCATT 1560
QY 1561 GCCGATCACCCGACCTTCCAGGCTCCACCTGCTGATGATGAGCAGGACGATCCTG 1620
Db 1561 GCCGATCACCCGACCTTCCAGGCTCCACCTGCTGATGATGAGCAGGACGATCCTG 1620
QY 1621 GATTACTTGGCAGATGTACCGTGAACAAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680
Db 1621 GATTACTTGGCAGATGTACCGTGAACAAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680
QY 1681 GCTCCTATCGATAAGCTGCTTAACATCAAGGATCTGCCACTGCCACGCGGTTCCCGTGAC 1740

Db 1681 GCTCTATCGATAAGCTGCCCTAACATCAAGGATCTGCCACTGCCACGCGTTCCCGTGAC 1740
QY 1741 CGCCTGAAGCAGCTTGGCCAGCGCGGTTTGGCTCGTGAATCTCCGTGAGCAGGACGCACTG 1800
Db 1741 CGCCTGAAGCAGCTTGGCCAGCGCGGTTTGGCTCGTGAATCTCCGTGAGCAGGACGCACTG 1800
QY 1801 GCAGTTACTGATACCACTTCCGCGATGCACACCAAGTCTTGTGTTGCGACCCGAGTCCGC 1860
Db 1801 GCAGTTACTGATACCACTTCCGCGATGCACACCAAGTCTTGTGTTGCGACCCGAGTCCGC 1860
QY 1861 TCATTCCGCACTGAAGCCTGCGGAGAGGCGCTCGCAAGCTGACTCCTGAGCTTTGTCC 1920
Db 1861 TCATTCCGCACTGAAGCCTGCGGAGAGGCGCTCGCAAGCTGACTCCTGAGCTTTGTCC 1920
QY 1921 GTGAGGCTTGGGCGGCGGAGCTACGATGTGGCGATGCGTTTCTCTTTGAGGATCCG 1980
Db 1921 GTGAGGCTTGGGCGGCGGAGCTACGATGTGGCGATGCGTTTCTCTTTGAGGATCCG 1980
QY 1981 TGGGACAGGCTCGACGAGCTGCGGAGGCGGATGCCGAATGTAACATTCAGATGCTGCTT 2040
Db 1981 TGGGACAGGCTCGACGAGCTGCGGAGGCGGATGCCGAATGTAACATTCAGATGCTGCTT 2040
QY 2041 CGCGGCGGCAACACCGTGGGATPACACCCCGTACCCAGACTCCGTCTGCGCGCGTTTGT 2100
Db 2041 CGCGGCGGCAACACCGTGGGATPACACCCCGTACCCAGACTCCGTCTGCGCGCGTTTGT 2100
QY 2101 AAGGAAGCTGCCAGCTCCGCGGCGGAGCATCTTCCGCACTTTCGACGCGCTTAACGACGTC 2160
Db 2101 AAGGAAGCTGCCAGCTCCGCGGCGGAGCATCTTCCGCACTTTCGACGCGCTTAACGACGTC 2160
QY 2161 TCCAGATGCGTCCAGCAATCGACGCGAGTCCCTGGAGACCAACACCGGTTAGCGGAGGTG 2220
Db 2161 TCCAGATGCGTCCAGCAATCGACGCGAGTCCCTGGAGACCAACACCGGTTAGCGGAGGTG 2220
QY 2221 GCTATGGCTTATTCTGGTGATCTCTGTATCCAAATGAAAGCTCTACACCCCTGGATTAC 2280
Db 2221 GCTATGGCTTATTCTGGTGATCTCTGTATCCAAATGAAAGCTCTACACCCCTGGATTAC 2280
QY 2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAAGAT 2340
Db 2281 TACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAAGAT 2340
QY 2341 ATGGCTGGTCTGCTTCGCCAGCTGCGGTAACCAAGTGGTCAACCGCACTGCGCGGTGAA 2400
Db 2341 ATGGCTGGTCTGCTTCGCCAGCTGCGGTAACCAAGTGGTCAACCGCACTGCGCGGTGAA 2400
QY 2401 TTCGATCTGCCAGTGCACGTCGACACCCAGCACTGCGGGTGGCCAGCTGGCAACCTAC 2460
Db 2401 TTCGATCTGCCAGTGCACGTCGACACCCAGCACTGCGGGTGGCCAGCTGGCAACCTAC 2460
QY 2461 TTTGTGTCAGCTCAAGCTGGTGAGATGCTGTTGACGGTGCTTCGCGCACCACTGTCTGGC 2520
Db 2461 TTTGTGTCAGCTCAAGCTGGTGAGATGCTGTTGACGGTGCTTCGCGCACCACTGTCTGGC 2520
QY 2521 ACCACCTCCAGCCATCCCTGTCTGCCATTGTTGCTGCTCATTCGCGCACACCCGTCCGGAT 2580
Db 2521 ACCACCTCCAGCCATCCCTGTCTGCCATTGTTGCTGCTCATTCGCGCACACCCGTCCGGAT 2580
QY 2581 ACCGTTTGAAGCTCGAGGCTGTTTCTGACCTCGAGGCGTACTGGGAAGCAGTGGCGGA 2640
Db 2581 ACCGTTTGAAGCTCGAGGCTGTTTCTGACCTCGAGGCGTACTGGGAAGCAGTGGCGGA 2640
QY 2641 CTGTACCTGCCATTGAGTCTGGAACCCAGGCCCAACCGGTGCGGTCTACCGCCACGAA 2700
Db 2641 CTGTACCTGCCATTGAGTCTGGAACCCAGGCCCAACCGGTGCGGTCTACCGCCACGAA 2700
QY 2701 ATCCAGGCGGACAGTTGTCCAACTGCGTGCAAGGCCACCGCACTGGGCTTGGCGAT 2760
Db 2701 ATCCAGGCGGACAGTTGTCCAACTGCGTGCAAGGCCACCGCACTGGGCTTGGCGAT 2760
QY 2761 CGTTTCGAAGCTCATCGAAGACAACTACGCGCCGTTAATGAGATGCTGGACGCCCAACC 2820

Db 2761 CGTTTCGAAGCTCATCGAAGACAACTACGCGCCGTTAATGAGATGCTGGACGCCCAACC 2820
QY 2821 AAGGTCACCCCATCCTCCAAAGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGGGGT 2880
Db 2821 AAGGTCACCCCATCCTCCAAAGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGGGGT 2880
QY 2881 GTGATCCAGCAGACTTTGTGCTCCGATCCACAAAAGTACGACATCCCGAGACTCTGTCTATC 2940
Db 2881 GTGATCCAGCAGACTTTGTGCTCCGATCCACAAAAGTACGACATCCCGAGACTCTGTCTATC 2940
QY 2941 GCGTTCCTGCGCGGCGAGCTTGGTAAACCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000
Db 2941 GCGTTCCTGCGCGGCGAGCTTGGTAAACCTCCAGGTGGCTGGCCAGAGCCACTGCGCACC 3000
QY 3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCTCTGAGGAAGAG 3060
Db 3001 CGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCTCTGAGGAAGAG 3060
QY 3061 CAGGCGCACCTCGACGCTGATGATTCCAAAGGAACGTGCAATAGCCTCAACCCGCTGCTG 3120
Db 3061 CAGGCGCACCTCGACGCTGATGATTCCAAAGGAACGTGCAATAGCCTCAACCCGCTGCTG 3120
QY 3121 TTCCGGAAGCCAAACCGAAGATTCTCTGAGCACCCGCTGCGCGCTTCGGCAACACCTCTGCG 3180
Db 3121 TTCCGGAAGCCAAACCGAAGATTCTCTGAGCACCCGCTGCGCGCTTCGGCAACACCTCTGCG 3180
QY 3181 CTGATGATCGTGAATTCTTCTACGGCCCTGGTCAAGGCCGCGGAGACTTTGATCCGCTCTG 3240
Db 3181 CTGATGATCGTGAATTCTTCTACGGCCCTGGTCAAGGCCGCGGAGACTTTGATCCGCTCTG 3240
QY 3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
Db 3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCTGGATGCGATCTCTGAGCCAGACGATAAG 3300
QY 3301 GGTATGCGCAATGTTGTGGCCAAACGTCAACCGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
Db 3301 GGTATGCGCAATGTTGTGGCCAAACGTCAACCGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
QY 3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGCGAGATTCTTCCAAACAAGGCCAT 3420
Db 3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGCGAGATTCTTCCAAACAAGGCCAT 3420
QY 3421 GTTGTGCAACCATTCGCTGGTGTGTACCGTGACTGTGCTGAAGGTGATGAGTCAAG 3480
Db 3421 GTTGTGCAACCATTCGCTGGTGTGTACCGTGACTGTGCTGAAGGTGATGAGTCAAG 3480
QY 3481 GCTGAGATGAGTGCATCATCGAGGCTATGAAGTGAAGCAACAATCACTGCTTCT 3540
Db 3481 GCTGAGATGAGTGCATCATCGAGGCTATGAAGTGAAGCAACAATCACTGCTTCT 3540
QY 3541 GTTGACGGCAAAATCGATCGCGTTGTGTTCCCTGCTGCAACGAAGGTGAAGTGGCGAC 3600
Db 3541 GTTGACGGCAAAATCGATCGCGTTGTGTTCCCTGCTGCAACGAAGGTGAAGTGGCGAC 3600
QY 3601 TTGATCGTCTGCTTTTCTTAA 3621
Db 3601 TTGATCGTCTGCTTTTCTTAA 3621

RESULT 5
AAH68526

ID AAH68526 standard; DNA; 349980 BP.

XX

AC AAH68526;

XX

DT 26-SEP-2001 (first entry)

XX

DE C glutamicum coding sequence fragment SEQ ID NO: 7061.

XX

KW Corynebacterium; amino acid synthesis; vitamin; saccharide;

XX organic acid synthesis; ds.

OS

Corynebacterium glutamicum.

XX EP1108790-A2.
PN 20-JUN-2001.
PD 18-DEC-2000; 2000EP-00127688.
XX 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX WPI; 2001-376931/40.
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX Disclosure; SEQ ID NO 7061; 246pp + Sequence Listing; English.
XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 349980 BP; 79274 A; 90638 C; 98727 G; 81341 T; 0 U; 0 Other;
Query Match 100.0%; Score 3621; DB 5; Length 349980;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGGGGCGGGTTAGATCCTGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGAGG 60
Db 105013 TGGGGCGGGTTAGATCCTGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGAGG 105072
QY 61 TCAGGGGAGTGTGCCCGAAACATTGAGAGGAAACAAACACCGATGTTTGAATGGGG 120
Db 105073 TCAGGGGAGTGTGCCCGAAACATTGAGAGGAAACAAACACCGATGTTTGAATGGGG 105132
QY 121 AATCGGGGTTACGATACCTAGGACGAGTACTGCTATCACCTTTGGCGGTCTCTTTGTTG 180
Db 105133 AATCGGGGTTACGATACCTAGGACGAGTACTGCTATCACCTTTGGCGGTCTCTTTGTTG 105192
QY 181 AAGGGAATAATTACTCTAGTGTGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
Db 105193 AAGGGAATAATTACTCTAGTGTGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 105252
QY 241 ATCTTGGTAGCAACCGCGGGAATCGCGTCCGTGCTTTCGGTGAGCACTCGAAACC 300
Db 105253 ATCTTGGTAGCAACCGCGGGAATCGCGTCCGTGCTTTCGGTGAGCACTCGAAACC 105312
QY 301 GGTGAGCCACGGTAGCTATTACCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 360
Db 105313 GGTGAGCCACGGTAGCTATTACCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT 105372
QY 361 GCTTCTGAAGCTGTCCGATTTGGTACCGAAGGTCACAGTCAAGGCGTACCTGGACATC 420
Db 105373 GCTTCTGAAGCTGTCCGATTTGGTACCGAAGGTCACAGTCAAGGCGTACCTGGACATC 105432
QY 421 GATGAAATTATCGGTGACGTAAAAAGTTAAAGCAGATGCCATTTACCGGGATACGGC 480

Db 105433 GATGAAATTATCGGTGACGCTAAAAAGTTAAAGCAGATGCCATTTACCGGGATACGGC 105492
QY 481 TTCCTGTCTGAAAAATGCCAGCTTGGCCGCGAGTGTGCGGAAAAACGGCATTTATTATT 540
Db 105493 TTCCTGTCTGAAAAATGCCAGCTTGGCCGCGAGTGTGCGGAAAAACGGCATTTATTATT 105552
QY 541 GGCCCAACCCAGAGTTCTTGATCTCAACCGTGATAAGTCTCGCGGGTAACCGCCGCG 600
Db 105553 GGCCCAACCCAGAGTTCTTGATCTCAACCGTGATAAGTCTCGCGGGTAACCGCCGCG 105612
QY 601 AAGAAGGCTGGTCTGCCAGTTTGGCGGAATCACCCCGAGCAAAAAACATCGATGAGATC 660
Db 105613 AAGAAGGCTGGTCTGCCAGTTTGGCGGAATCACCCCGAGCAAAAAACATCGATGAGATC 105672
QY 661 GTTAAAAAGCGCTGAAGCCAGACTTACCCCATCTTTGTGAAGGCGAGTTGCCGTGGTGGC 720
Db 105673 GTTAAAAAGCGCTGAAGCCAGACTTACCCCATCTTTGTGAAGGCGAGTTGCCGTGGTGGC 105732
QY 721 GGACGCGGTATGCGTTTGTGCTTTCACCTGATGAGCTTCGCAAAATTAGCAACAGAAGCA 780
Db 105733 GGACGCGGTATGCGTTTGTGCTTTCACCTGATGAGCTTCGCAAAATTAGCAACAGAAGCA 105792
QY 781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTGCAACGTGTGTGATT 840
Db 105793 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTGCAACGTGTGTGATT 105852
QY 841 AACCTCAGCATATTGAAGTGAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
Db 105853 AACCTCAGCATATTGAAGTGAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 105912
QY 901 TATGAACGTGACTGCTCACTGAGCGTCTGTCAACCAAAAGTTGTGCAAAATTGCGCCAGCA 960
Db 105913 TATGAACGTGACTGCTCACTGAGCGTCTGTCAACCAAAAGTTGTGCAAAATTGCGCCAGCA 105972
QY 961 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAATAAGTTCTGCGC 1020
Db 105973 CAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAATAAGTTCTGCGC 106032
QY 1021 TCCATTGTTTACAGGGCGCGGAAACCGTGAATTTCTGTCGATGAAAAGGGCAACCAC 1080
Db 106033 TCCATTGTTTACAGGGCGCGGAAACCGTGAATTTCTGTCGATGAAAAGGGCAACCAC 106092
QY 1081 GTCTTCATCGAAATGAACCCACGTATCCAGTTTGAAGCAACCGTGAAGTGAAGTCAAC 1140
Db 106093 GTCTTCATCGAAATGAACCCACGTATCCAGTTTGAAGCAACCGTGAAGTGAAGTCAAC 106152
QY 1141 GAGTGGACCTGGTGAAGCGCGAGATGCGCTTGGCTGCTGTCGCAACCTTGAAGGAATTG 1200
Db 106153 GAGTGGACCTGGTGAAGCGCGAGATGCGCTTGGCTGCTGTCGCAACCTTGAAGGAATTG 106212
QY 1201 GGTCTGACCCCAAGATAAGATCAAGACCCACCGTGCAGCACTGAGTCCCGCATCACCACG 1260
Db 106213 GGTCTGACCCCAAGATAAGATCAAGACCCACCGTGCAGCACTGAGTCCCGCATCACCACG 106272
QY 1261 GAAGATCCAAACAACCGCTTCCGCCCAAGATACCGGAACATATACCGCGTACCGCTCACCA 1320
Db 106273 GAAGATCCAAACAACCGCTTCCGCCCAAGATACCGGAACATATACCGCGTACCGCTCACCA 106332
QY 1321 GGCGGAGCTGGCGTTCGTCTTGACCGTGCAGCTCAGCTCGGTGCGGAAATCACCGCACAC 1380
Db 106333 GGCGGAGCTGGCGTTCGTCTTGACCGTGCAGCTCAGCTCGGTGCGGAAATCACCGCACAC 106392
QY 1381 TTTGACTCCATGCTGGTGAATAATGACCTGCGGTGTTCCGACTTTGAAAACCTGCTGTTGCT 1440
Db 106393 TTTGACTCCATGCTGGTGAATAATGACCTGCGGTGTTCCGACTTTGAAAACCTGCTGTTGCT 106452
QY 1441 CGTGACAGCGCGGTGGCTGAGTTCAACCGTGTCTGCTGTTTGAACCAACATTTGTTTC 1500
Db 106453 CGTGACAGCGCGGTGGCTGAGTTCAACCGTGTCTGCTGTTTGAACCAACATTTGTTTC 106512
QY 1501 TTGCGTGGCTTGTGCGGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTTCATT 1560
Db 106513 TTGCGTGGCTTGTGCGGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTTCATT 106572

QY 1561 GCGGATCACCCGACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGACGCATCCTG 1620
Db 106573 GCGGATCACCCGACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGACGCATCCTG 106632
QY 1621 GATTACTTGGCAGATGTCAACCGTGAAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 1680
Db 106633 GATTACTTGGCAGATGTCAACCGTGAAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCA 106692
QY 1681 GCTCCTATCGATAAGCTGCTTAACATCAAGGATCTGCCACTGCCACGCGTTCCTCGTGAC 1740
Db 106693 GCTCCTATCGATAAGCTGCTTAACATCAAGGATCTGCCACTGCCACGCGTTCCTCGTGAC 106752
QY 1741 CGCTGAAGCAGCTTGGCCAGCCGCGTTCCTGCTGATCTCCGTGAGCAGGACGCACCTG 1800
Db 106753 CGCTGAAGCAGCTTGGCCAGCCGCGTTCCTGCTGATCTCCGTGAGCAGGACGCACCTG 106812
QY 1801 GCAGTTACTGATACCACTTCGCGGATGCACACCACTCTTTCCTGAGCAGGACGCACCTG 1860
Db 106813 GCAGTTACTGATACCACTTCGCGGATGCACACCACTCTTTCCTGAGCAGGACGCACCTG 106872
QY 1861 TCATTCGCACTGAAGCCTTCGCGGAGAGGCGCTCCGAAAGCTGACTCCTGAGCTTTTGTCC 1920
Db 106873 TCATTCGCACTGAAGCCTTCGCGGAGAGGCGCTCCGAAAGCTGACTCCTGAGCTTTTGTCC 106932
QY 1921 GTGAGGCCCTGGGGCGGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 1980
Db 106933 GTGAGGCCCTGGGGCGGCGACCTACGATGTGGCGATGCGTTTCCTCTTTGAGGATCCG 106992
QY 1981 TGGGACAGGCTCGACGAGTGGCGGAGGCGATGCGAAATGTAACATTTCAGATGCTGCTT 2040
Db 106993 TGGGACAGGCTCGACGAGTGGCGGAGGCGATGCGAAATGTAACATTTCAGATGCTGCTT 107052
QY 2041 CGCGGCCGCAACACCCGTGGGATACACCCCGTACCCAGACTCCGTCGCGCGCGTTTGT 2100
Db 107053 CGCGGCCGCAACACCCGTGGGATACACCCCGTACCCAGACTCCGTCGCGCGCGTTTGT 107112
QY 2101 AAGGAAGCTGCCAGCTCCGCGTGGACATCTTCGCGATCTTCGACGCGGTTAACGACGTC 2160
Db 107113 AAGGAAGCTGCCAGCTCCGCGTGGACATCTTCGCGATCTTCGACGCGGTTAACGACGTC 107172
QY 2161 TCCAGATGCGTCCAGCAATCGACGCGAGTCTTGAGACCAACACCGCGGTAGCCGAGGTG 2220
Db 107173 TCCAGATGCGTCCAGCAATCGACGCGAGTCTTGAGACCAACACCGCGGTAGCCGAGGTG 107232
QY 2221 GCTATGGCTTATCTGTGATCTCTCTGATCCAAATGAAGCTCTACACCTGGATTAC 2280
Db 107233 GCTATGGCTTATCTGTGATCTCTCTGATCCAAATGAAGCTCTACACCTGGATTAC 107292
QY 2281 TACCTAAAGATGGCAGAGAGATCGTCAAGCTGGCGCTCACATCTTGGCCATTAAAGAT 2340
Db 107293 TACCTAAAGATGGCAGAGAGATCGTCAAGCTGGCGCTCACATCTTGGCCATTAAAGAT 107352
QY 2341 ATGGCTGGTCTGCTTCGCCAGCTGCGGTAAACCAAGCTGGTCACCGCACTGCGCCGTGAA 2400
Db 107353 ATGGCTGGTCTGCTTCGCCAGCTGCGGTAAACCAAGCTGGTCACCGCACTGCGCCGTGAA 107412
QY 2401 TTCGATCTGCCAGTGCAAGTGCAACCCAGCACTGCGGTGGCCAGCTGGCAACCTAC 2460
Db 107413 TTCGATCTGCCAGTGCAAGTGCAACCCAGCACTGCGGTGGCCAGCTGGCAACCTAC 107472
QY 2461 TTTGCTGCAGCTCAAGCTGGTGAGATGCTGTGACGGTGTTCGCGACCACTGTCTGGC 2520
Db 107473 TTTGCTGCAGCTCAAGCTGGTGAGATGCTGTGACGGTGTTCGCGACCACTGTCTGGC 107532
QY 2521 ACCACCTCCAGCCATCCCTGTCTGCCATTGTTGTCATTCGCGCACACCCGTCGCGAT 2580
Db 107533 ACCACCTCCAGCCATCCCTGTCTGCCATTGTTGTCATTCGCGCACACCCGTCGCGAT 107592
QY 2581 ACCGGTTTGAAGCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCAGGGA 2640
Db 107593 ACCGGTTTGAAGCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCAGGGA 107652

QY 2641 CTGTACCTGCCATTGAGTCTGGAAACCCAGGCCCCAACCGGTGCGTCTACCGCCACGAA 2700
Db 107653 CTGTACCTGCCATTGAGTCTGGAAACCCAGGCCCCAACCGGTGCGTCTACCGCCACGAA 107712
QY 2701 ATCCAGGCGGACAGTTGTCAAACCTGCGTGACAGGCCACCGCAGCTGGGCTTGGGAT 2760
Db 107713 ATCCAGGCGGACAGTTGTCAAACCTGCGTGACAGGCCACCGCAGCTGGGCTTGGGAT 107772
QY 2761 CGTTTCGAACCTCATCGAAGACAACTACGAGCCGTTAAATGAGATGCTGGAGCGCCAAAC 2820
Db 107773 CGTTTCGAACCTCATCGAAGACAACTACGAGCCGTTAAATGAGATGCTGGAGCGCCAAAC 107832
QY 2821 AAGGTACCCCATCTTCGAAGGTTGTTGGGACCTCGCACTCCACCTCGTTGGTGGGT 2880
Db 107833 AAGGTACCCCATCTTCGAAGGTTGTTGGGACCTCGCACTCCACCTCGTTGGTGGGT 107892
QY 2881 GTGGATCCAGCAGACTTTCGTCGCGATCCACAAAAGTACGACATCCAGACTCTGTCTATC 2940
Db 107893 GTGGATCCAGCAGACTTTCGTCGCGATCCACAAAAGTACGACATCCAGACTCTGTCTATC 107952
QY 2941 GCGTTCCTGCGCGGCGAGCTTGGTAAACCTCCAGGTGGTGGCCAGAGCCACTGCGCAC 3000
Db 107953 GCGTTCCTGCGCGGCGAGCTTGGTAAACCTCCAGGTGGTGGCCAGAGCCACTGCGCAC 108012
QY 3001 CGCGCACTGGAAGCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCTGAGGAAGAG 3060
Db 108013 CGCGCACTGGAAGCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCTGAGGAAGAG 108072
QY 3061 CAGCGCACCTCGACGCTGATGATTCGAAGGCAAGGCACCTCTGACGGAAGTTCTGAGGAAGAG 3120
Db 108073 CAGCGCACCTCGACGCTGATGATTCGAAGGCAAGGCACCTCTGACGGAAGTTCTGAGGAAGAG 108132
QY 3121 TTCCGGAAGCCAAACCGAAGAGTTCTTCGAGCACCGTCGCGCTTCGGCAACACCTCTGCG 3180
Db 108133 TTCCGGAAGCCAAACCGAAGAGTTCTTCGAGCACCGTCGCGCTTCGGCAACACCTCTGCG 108192
QY 3181 CTGGATGATCGTGAAATTTCTACGGCTGTTGTTGCGCTGTTGCGAGCTTTGATCCGCTG 3240
Db 108193 CTGGATGATCGTGAAATTTCTACGGCTGTTGTTGCGCTGTTGCGAGCTTTGATCCGCTG 108252
QY 3241 CCAGATGTGCGCACCCCACTGTTGTTGCGCTGTTGTTGCGATCTCTGAGCCAGACGATAAG 3300
Db 108253 CCAGATGTGCGCACCCCACTGTTGTTGCGCTGTTGTTGCGATCTCTGAGCCAGACGATAAG 108312
QY 3301 GGTATCGCAATGTTGTGGCCAAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
Db 108313 GGTATCGCAATGTTGTGGCCAAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 108372
QY 3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGCGAGTTCTCTCCAAAGGGCCAT 3420
Db 108373 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGCGAGTTCTCTCCAAAGGGCCAT 108432
QY 3421 GTTGTGCACCAATTCGCTGGTGTGTCAACCGTACTGTTGCTGAAGGTGATGAGGTCAAG 3480
Db 108433 GTTGTGCACCAATTCGCTGGTGTGTCAACCGTACTGTTGCTGAAGGTGATGAGGTCAAG 108492
QY 3481 GCTGAGATGCACTCGCAATCATCGAGGCTATGAAGATGGAAGCAACATCACTGCTTCT 3540
Db 108493 GCTGAGATGCACTCGCAATCATCGAGGCTATGAAGATGGAAGCAACATCACTGCTTCT 108552
QY 3541 GTTGACGGCAAAATCGATCGCGTGTGTTCTGCTGCAACGAAAGGTGGAAGGTGGCGAC 3600
Db 108553 GTTGACGGCAAAATCGATCGCGTGTGTTCTGCTGCAACGAAAGGTGGAAGGTGGCGAC 108612
QY 3601 TTGATCGTCTGTTTCCTAA 3621
Db 108613 TTGATCGTCTGTTTCCTAA 108633

RESULT 6
AAX24102
ID AAX24102 standard; DNA; 3728 BP.
XX

AC AAX24102;
XX
DT 30-JUN-1999 (first entry)
XX
DE C. glutamicum pyruvate carboxylase genomic DNA.
XX
KW Pyruvate carboxylase; amino acid production; lysine production;
KW threonine production; homoserine production; glutamate production;
KW arginine production; feed additive; condiment; pharmaceutical;
KW fine chemical; ss.
XX
OS Corynebacterium glutamicum.
XX
FH Key Location/Qualifiers
FT CDS 165..3587
FT /*tag= a
FT /product= "pyruvate carboxylase"
XX
PN DE19831609-A1.
XX
PD 15-APR-1999.
XX
PF 14-JUL-1998; 98DE-01031609.
XX
PR 04-OCT-1997; 97DE-01043894.
XX
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI Peters-Wendisch P, Eikmanns B, Sahn H;
XX
DR WPI; 1999-245521/21.
DR P-PSDB; AAW93971.
XX
XX
PT Increasing microbial production of specific amino acids by increasing
PT activity or expression of pyruvate carboxylase.
XX
PS Claim 16; Page 8-11; 18pp; German.
XX
CC This invention describes the isolation of a pyruvate carboxylase from
CC Corynebacterium glutamicum which is used in a novel method for production
CC of lysine, threonine, homoserine, glutamate and/or arginine, variously
CC useful as feed additives, condiments, pharmaceuticals and intermediates
CC for fine chemicals. Increasing pyruvate carboxylase activity increases
CC the yield of microbial production of amino acids of the aspartate and/or
CC glutamate families, e.g. about 50% more lysine, 40% more threonine and
CC 150% more homoserine are secreted into the culture medium
XX
SQ Sequence 3728 BP; 813 A; 1059 C; 1035 G; 821 T; 0 U; 0 Other;
Query Match 98.8%; Score 3576.4; DB 2; Length 3728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3577; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 44 GCTTGAAGTCGTGCAGGTGAGGGAGTGTGCGGAAACATTGAGAGGAAACAAAC 103
Db 10 GCTTGAAGTCGTGCAGGTGAGGGAGTGTGCGGAAACATTGAGAGGAAACAAAC 69
QY 104 CGATGTTGATTGGGGGAATCGGGGTTACGATACTAGGACGAGTGACTGCTATCACCC 163
Db 70 CGATGTTGATTGGGGGAATCGGGGTTACGATACTAGGACGAGTGACTGCTATCACCC 129
QY 164 TTGGCGGTCTCTGTTGAAAGGAATAATTACTAGTGTGACTCACACATCTTCAACGC 223
Db 130 TTGGCGGTCTCTGTTGAAAGGAATAATTACTAGTGTGACTCACACATCTTCAACGC 189
QY 224 TTCCAGCATTCAAAAGATCTTGGTAGCAACCGCGGGAATCGGGTCCGTGCTTTCC 283
Db 190 TTCCAGCATTCAAAAGATCTTGGTAGCAACCGCGGGAATCGGGTCCGTGCTTTCC 249
QY 284 GTGCAGCACTCGAAACCGGTGACCCACGGTAGCTATTACCCCGGTGAAGATCGGGAT 343
Db 250 GTGCAGCACTCGAAACCGGTGACCCACGGTAGCTATTACCCCGGTGAAGATCGGGAT 309

QY 344 CATTCCACCGCTCTTTTGTCTTGAAGCTGTCGCAATGGTACCGAAGGCTCACCAGTCA 403
Db 310 CATTCCACCGCTCTTTTGTCTTGAAGCTGTCGCAATGGTACCGAAGGCTCACCAGTCA 369
QY 404 AGCGTACCTGGACATCGATGAAATATCGGTGAGCTAAAAAGTTAAAGCAGATGCCA 463
Db 370 AGCGTACCTGGACATCGATGAAATATCGGTGAGCTAAAAAGTTAAAGCAGATGCCA 429
QY 464 TTTACCCGGGATACGGCTTCTGTCTGAAAAATGCCAGCTTGCCTGCGAGTGTGGGAAA 523
Db 430 TTTACCCGGGATACGGCTTCTGTCTGAAAAATGCCAGCTTGCCTGCGAGTGTGGGAAA 489
QY 524 ACGGCATTAATTTATTGGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTC 583
Db 490 ACGGCATTAATTTATTGGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTC 549
QY 584 GCGCGTAACCGCGCGAAGAGGCTGGTCTGCCAGTTTGGCGGAATCCACCCGAGCA 643
Db 550 GCGCGTAACCGCGCGAAGAGGCTGGTCTGCCAGTTTGGCGGAATCCACCCGAGCA 609
QY 644 AAAACATCGATGAGATCGTTAAAAAGCGCTGAAGCCAGACTTACCCCATCTTTGTGAAGG 703
Db 610 AAAACATCGATGAGATCGTTAAAAAGCGCTGAAGCCAGACTTACCCCATCTTTGTGAAGG 669
QY 704 CAGTTGCCGGTGGTGGCGAGCGGGTATGCGTTTGTGTTTGTCTTCACTGATGAGCTTCGCA 763
Db 670 CAGTTGCCGGTGGTGGCGAGCGGGTATGCGTTTGTGTTTGTCTTCACTGATGAGCTTCGCA 729
QY 764 AATTAGCAACAGAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGSCGCGGTATATG 823
Db 730 AATTAGCAACAGAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGSCGCGGTATATG 789
QY 824 TCGAACGTGCTGTGATTAAACCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTG 883
Db 790 TCGAACGTGCTGTGATTAAACCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTG 849
QY 884 GAGAAATTGTACACCTTTATGAACGTGACTGCTCACTGACGCTCGTCACCAAAAAAGTTG 943
Db 850 GAGAAATTGTACACCTTTATGAACGTGACTGCTCACTGACGCTCGTCACCAAAAAAGTTG 909
QY 944 TCGAATTTGCCCGCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTTGTGCGGATG 1003
Db 910 TCGAATTTGCCCGCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTTGTGCGGATG 969
QY 1004 CAGTAAAGTTCTGCCGCTCCATTGTTTACCAGGGCGCGGAAACCGTGGAATTTTGGTCG 1063
Db 970 CAGTAAAGTTCTGCCGCTCCATTGTTTACCAGGGCGCGGAAACCGTGGAATTTTGGTCG 1029
QY 1064 ATGAAAAGGGCAACCACTTTTCATCGAAATGAACCCACGTATCCAGGTTGACACACCG 1123
Db 1030 ATGAAAAGGGCAACCACTTTTCATCGAAATGAACCCACGTATCCAGGTTGACACACCG 1089
QY 1124 TGACTGAAGAAAGTCAACGAGTGGACCTGGTGAAGCGCGCAGATGCGCTTGGCTGCTGGTG 1183
Db 1090 TGACTGAAGAAAGTCAACGAGTGGACCTGGTGAAGCGCGCAGATGCGCTTGGCTGCTGGTG 1149
QY 1184 CAACCTTGAAGGAATTGGTCTGACCCAAAGATAAGATCAAGACCCACGCGTGACGACTGC 1243
Db 1150 CAACCTTGAAGGAATTGGTCTGACCCAAAGATAAGATCAAGACCCACGCGTGACGACTGC 1209
QY 1244 AGTGCCGCATCACCAAGGAAGATCCAAACAAACCGCTTCCGCCAGATACCGGAACATCA 1303
Db 1210 AGTGCCGCATCACCAAGGAAGATCCAAACAAACCGCTTCCGCCAGATACCGGAACATCA 1269
QY 1304 CCGCGTACCGCTCACAGCGGAGCTGGCGTTTCGTTTGAACGCTGAGCTCAGCTCGGTG 1363
Db 1270 CCGCGTACCGCTCACAGCGGAGCTGGCGTTTCGTTTGAACGCTGAGCTCAGCTCGGTG 1329
QY 1364 GCGAAATCACCGCACATTTTGAATCCATGCTGGTGAATGACCTGCCGTGGTTCGACT 1423
Db 1330 GCGAAATCACCGCACATTTTGAATCCATGCTGGTGAATGACCTGCCGTGGTTCGACT 1389
QY 1424 TTGAAACTGCTGTTGCTGCTGACAGCGCGGCTTGGGTGAGTTTCAACCGTGTCTGGTGTG 1483

Db 1390 TTGAAACTGCTGTTGCTCGTGACAGCGCGGCTTGGCTGAGTTTACCGTGTCTGGTGTG 1449
Qy 1484 CAACCAACATTGTTGCTGCGTTCGTTGCTGCGGGAAGAGGACTTCACTTCCAAAGCGCA 1543
Db 1450 CAACCAACATTGTTGCTGCGTTCGTTGCTGCGGGAAGAGGACTTCACTTCCAAAGCGCA 1509
Qy 1544 TCGCCACCGGATTCAATGCCGATCACCCGACCTCTTTCAGGCTCCACCTGCTGATGATG 1603
Db 1510 TCGCCACCGGATTCAATGCCGATCACCCGACCTCTTTCAGGCTCCACCTGCTGATGATG 1569
Qy 1604 AGCAGGGACGATCCTGGATTACTTGGCAGATGTCAACCGTGAACAAAGCCTCATGGTGTGC 1663
Db 1570 AGCAGGGAGGATCCTGGATTACTTGGCAGATGTCAACCGTGAACAAAGCCTCATGGTGTGC 1629
Qy 1664 GTCCAAAGGATTGTCAGCTCCTATCGATAAGCTGCCCTAAACATCAAGGATCGCCACTGC 1723
Db 1630 GTCCAAAGGATTGTCAGCTCCTATCGATAAGCTGCCCTAAACATCAAGGATCGCCACTGC 1689
Qy 1724 CACGCGGTTCCCGTGACCGCTGAAGCAGCTTGGCCCGAGCCGCTTGGCTCGTGAATCCTC 1783
Db 1690 CACGCGGTTCCCGTGACCGCTGAAGCAGCTTGGCCCGAGCCGCTTGGCTCGTGAATCCTC 1749
Qy 1784 GTGAGCAGGACGCACTGGCAGTTACTGATACCACTTCCGCGATGACACACAGCTTTTGC 1843
Db 1750 GTGAGCAGGACGCACTGGCAGTTACTGATACCACTTCCGCGATGACACACAGCTTTTGC 1809
Qy 1844 TTGCGACCCGAGTCCGCTCATTCGCACTGAAGCTGCGGCGAGGCGCTCGCAAAGCTGA 1903
Db 1810 TTGCGACCCGAGTCCGCTCATTCGCACTGAAGCTGCGGCGAGGCGCTCGCAAAGCTGA 1869
Qy 1904 CTCCTGAGCTTTTGTCCGTGGAGGCTTGGGCGCGCGGACCTACGATGTCGCGATGCGTT 1963
Db 1870 CTCCTGAGCTTTTGTCCGTGGAGGCTTGGGCGCGCGGACCTACGATGTCGCGATGCGTT 1929
Qy 1964 TCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGGAGGCGGATGCCGAATGTAA 2023
Db 1930 TCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGGAGGCGGATGCCGAATGTAA 1989
Qy 2024 ACATTGAGATGCTGCTCGCGGCGGCAACACCGTGGGATACACCCCGTACCCAGACTCCG 2083
Db 1990 ACATTGAGATGCTGCTCGCGGCGGCAACACCGTGGGATACACCCCGTACCCAGACTCCG 2049
Qy 2084 TCTGCCGCGGCTTTGTTAAGGAAGCTGCCAGCTCCGCGGTGGACATCTTCCGCTCTTCG 2143
Db 2050 TCTGCCGCGGCTTTGTTAAGGAAGCTGCCAGCTCCGCGGTGGACATCTTCCGCTCTTCG 2109
Qy 2144 ACGCGCTTAAACGAGTCTCCAGATGCGTCCAGCAATCGACGAGTCTCTGGAGACCAACA 2203
Db 2110 ACGCGCTTAAACGAGTCTCCAGATGCGTCCAGCAATCGACGAGTCTCTGGAGACCAACA 2169
Qy 2204 CCGCGGTAGCCGAGGTGGCTATGGCTTATTTCTGGTATCTCTCTGATCCAAATGAAAAGC 2263
Db 2170 CCGCGGTAGCCGAGGTGGCTATGGCTTATTTCTGGTATCTCTCTGATCCAAATGAAAAGC 2229
Qy 2264 TCTACACCTGGATTACTACCTAAAGATGGCAGAGAGATCGTCAAGTCTGGCGCTCACA 2323
Db 2230 TCTACACCTGGATTACTACCTAAAGATGGCAGAGAGATCGTCAAGTCTGGCGCTCACA 2289
Qy 2324 TCTTGGCCATTAAAGGATATGGCTGGTCTGCTTCCGCCAGCTGCGGTAAACAAAGCTGGTCA 2383
Db 2290 TCTTGGCCATTAAAGGATATGGCTGGTCTGCTTCCGCCAGCTGCGGTAAACAAAGCTGGTCA 2349
Qy 2384 CCGCACTGCGCGGTGAATTCGATCTGCCAGTGCAGTGCACACCCACGACTGCGGGTG 2443
Db 2350 CCGCACTGCGCGGTGAATTCGATCTGCCAGTGCAGTGCACACCCACGACTGCGGGTG 2409
Qy 2444 GCCAGCTGGCAACCTACTTTGCTGTCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGT 2503
Db 2410 GCCAGCTGGCAACCTACTTTGCTGTCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGT 2469
Qy 2504 CCGCACCACTGTCTGGCACCACTCCAGCCATCCCTGTCTGCCATTGTTGCTGCTCAT 2563

Db 2470 CCGCACCACTGTCTGGCACCACTCCAGCCATCCCTGTCTGCCATTGTTGCTGCTATTCG 2529
Qy 2564 CGCACACCCGTCGCGATACCGGTTTTCAGCTTCGAGGCTGTTTCTGACCTCGAGCCGCTACT 2623
Db 2530 CGCACACCCGTCGCGATACCGGTTTTCAGCTTCGAGGCTGTTTCTGACCTCGAGCCGCTACT 2589
Qy 2624 GGAAGCAGTGCAGGCTGTACCTGCCATTTCAGTCTGGAACCCAGGCCCCAACCGGTC 2683
Db 2590 GGAAGCAGTGCAGGCTGTACCTGCCATTTCAGTCTGGAACCCAGGCCCCAACCGGTC 2649
Qy 2684 GCGTCTACCCGCCACGAAATCCAGGCGGACAGTTGTCCAACTGCGTGCACAGGCCACCG 2743
Db 2650 GCGTCTACCCGCCACGAAATCCAGGCGGACAGTTGTCCAACTGCGTGCACAGGCCACCG 2709
Qy 2744 CACTGGGCTTTCGCGATCGTTTCGAACCTCATCGAAGACAACTACGACGCGTTAATGAGA 2803
Db 2710 CACTGGGCTTTCGCGATCGTTTCGAACCTCATCGAAGACAACTACGACGCGTTAATGAGA 2769
Qy 2804 TGCTGGGACGCCCAACCAAGGTCAACCCCATCTTCCAAGTTGTTGSGGACCTCGCACTCC 2863
Db 2770 TGCTGGGACGCCCAACCAAGGTCAACCCCATCTTCCAAGTTGTTGSGGACCTCGCACTCC 2829
Qy 2864 ACCTCGTTGGTCCGGTGTGGATCCAGCAGACTTGTGCTGCCGATCCACAAAGTACGACA 2923
Db 2830 ACCTCGTTGGTCCGGTGTGGATCCAGCAGACTTGTGCTGCCGATCCACAAAGTACGACA 2889
Qy 2924 TCCAGACTCTGTCTCATCGCGTTCTTCCGCGGCGAGCTTGGTAACCTTCCAGGTGGCTGGC 2983
Db 2890 TCCAGACTCTGTCTCATCGCGTTCTTCCGCGGCGAGCTTGGTAACCTTCCAGGTGGCTGGC 2949
Qy 2984 CAGAGCCACTGCGCACCCGCGCACTGGGAAGGCGCTCCGAAGGCAAGGCACCTCTGACCG 3043
Db 2950 CAGAGCCACTGCGCACCCGCGCACTGGGAAGGCGCTCCGAAGGCAAGGCACCTCTGACCG 3009
Qy 3044 AAGTTCTGTAGGAAGAGCAGGCGCACTTGAACGCTGATGATTCCAAGGAACGTCGCAATA 3103
Db 3010 AAGTTCTGTAGGAAGAGCAGGCGCACTTGAACGCTGATGATTCCAAGGAACGTCGCAATA 3069
Qy 3104 GCCTCAACCGCTGCTGTTCCGAAGCCAAACCGAAGAGTTCTCTCGAGAACGTCGCGCT 3163
Db 3070 GCCTCAACCGCTGCTGTTCCGAAGCCAAACCGAAGAGTTCTCTCGAGAACGTCGCGCT 3129
Qy 3164 TCGGCAACACCTCTGCGCTGGATGATCGTGAATTTCTACGGCTTGTTCGAAGGCCCGCG 3223
Db 3130 TCGGCAACACCTCTGCGCTGGATGATCGTGAATTTCTACGGCTTGTTCGAAGGCCCGCG 3189
Qy 3224 AGACTTTGATCCGCTGCCAGATGTGCGCACCCACTGCTTGTTCGCTGGATGCGATCT 3283
Db 3190 AGACTTTGATCCGCTGCCAGATGTGCGCACCCACTGCTTGTTCGCTGGATGCGATCT 3249
Qy 3284 CTGAGCCAGACGATTAAGGATGCGCAATGTTGTCGCAACGTCGCAAGGCGGATCCGCC 3343
Db 3250 CTGAGCCAGACGATTAAGGATGCGCAATGTTGTCGCAACGTCGCAAGGCGGATCCGCC 3309
Qy 3344 CAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCTACCGCAACCGCAGAAAAGGCGAGATT 3403
Db 3310 CAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCTACCGCAACCGCAGAAAAGGCGAGATT 3369
Qy 3404 CCTCCAACAAAGGCGCATGTTGCTGCACCATTCGCTGGTGTGTACCGCTGACTGTTGCTG 3463
Db 3370 CCTCCAACAAAGGCGCATGTTGCTGCACCATTCGCTGGTGTGTACCGCTGACTGTTGCTG 3429
Qy 3464 AAGGTGATGAGGTCAAGGCTGGAGATGCAGTCCGAATCATCGAGGCTATGAAGATGGAAG 3523
Db 3430 AAGGTGATGAGGTCAAGGCTGGAGATGCAGTCCGAATCATCGAGGCTATGAAGATGGAAG 3489
Qy 3524 CAACAATCACTGCTTCTGTTGACGGCAAAATCGATCGCTTGTGTTCTCTGCTGCAACGA 3583
Db 3490 CAACAATCACTGCTTCTGTTGACGGCAAAATCGATCGCTTGTGTTCTCTGCTGCAACGA 3549
Qy 3584 AGGTGGAAGGTGGCGACTTGATCGTCTGTTTCTCTAA 3621
Db 3550 AGGTGGAAGGTGGCGACTTGATCGTCTGTTTCTCTAA 3587

RESULT 7
AAH65730
ID AAH65730 standard; DNA; 3420 BP.
XX
AC AAH65730;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 765.
XX
XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
FN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
(KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
DR P-PSDB; AAG90511.
XX

Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
XX
PS Claim 8; SEQ ID NO 765; 246pp + Sequence Listing; English.
XX

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office

SQ Sequence 3420 BP; 732 A; 1004 C; 939 G; 745 T; 0 U; 0 Other;

Query Match 94.4%; Score 3420; DB 5; Length 3420;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 GTGTGACTCACACATCTTCAACGCTTCCAGCATTCAAAAGATCTTGGTAGCAACCGC 258
Db 1 GTGTGACTCACACATCTTCAACGCTTCCAGCATTCAAAAGATCTTGGTAGCAACCGC 60
QY 259 GCGGAAATCGCGTCCGTGCTTTCCGTGAGCACTCGAAACCGGTGCAGCCACGCTAGCT 318
Db 61 GCGGAAATCGCGTCCGTGCTTTCCGTGAGCACTCGAAACCGGTGCAGCCACGCTAGCT 120
QY 319 ATTTACCCCGTGAAGATCGGGATCATTCACCGCTCTTTTGTCTTGAAGCTGTCCGC 378
Db 121 ATTTACCCCGTGAAGATCGGGATCATTCACCGCTCTTTTGTCTTGAAGCTGTCCGC 180
QY 379 ATTGGTACCGAGGCTCACCGATCAAGGCGTACCTGGACATCGATGAATATCGGTGCA 438

Db 181 ATGTGTACCGAAGGCTCACAGTCAAGGCGTACCTGGACATCGATGAAATATCGGTGCA 240
QY 439 GCTAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCTGTCTGAAAAATGCC 498
Db 241 GCTAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCTGTCTGAAAAATGCC 300
QY 499 CAGCTTGCCTCGGAGTGTGGGAAAAACGGCATTACTTTTATTGGCCCCAACCCACAGAGTT 558
Db 301 CAGCTTGCCTCGGAGTGTGGGAAAAACGGCATTACTTTTATTGGCCCCAACCCACAGAGTT 360
QY 559 CTTGATCTCACCGGTGATAAGTCTCGCGGGTAAACCGCGGGAAGAGCTGTCTGCCA 618
Db 361 CTTGATCTCACCGGTGATAAGTCTCGCGGGTAAACCGCGGGAAGAGCTGTCTGCCA 420
QY 619 GTTTTGGCGGAATCCACCCGAGCAAAAACATCGATGAGATCGTTAAAAAGCGCTGAAGGC 678
Db 421 GTTTTGGCGGAATCCACCCGAGCAAAAACATCGATGAGATCGTTAAAAAGCGCTGAAGGC 480
QY 679 CAGACTTACCCCATCTTTGTGAAGGCAGTTGCGGTGGTGGGACGCGGTATGCGTTT 738
Db 481 CAGACTTACCCCATCTTTGTGAAGGCAGTTGCGGTGGTGGGACGCGGTATGCGTTT 540
QY 739 GTTGTCTCACCTGATGAGCTTCGCAAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCG 798
Db 541 GTTGTCTCACCTGATGAGCTTCGCAAAATTAGCAACAGAAGCATCTCGTGAAGCTGAAGCG 600
QY 799 GCTTTCGCGGATGGCGGTATATGTGAAAGTTCGAAAGTCTGTGATTAACCCCTCAGCATATTGAA 858
Db 601 GCTTTCGCGGATGGCGGTATATGTGAAAGTTCGAAAGTTCGAAAGTTCGAAAGTTCGAAAG 660
QY 859 GTGCAGATCCTTTGGCGATCACACTGGAGAAAGTTGTACACCTTTATGAACGTGACTGCTCA 918
Db 661 GTGCAGATCCTTTGGCGATCACACTGGAGAAAGTTGTACACCTTTATGAACGTGACTGCTCA 720
QY 919 CTGCAGCTGCTCACCAAAAAGTTGTGAAATTTGCGCCAGCACAGCATTTGGATCCAGAA 978
Db 721 CTGCAGCTGCTCACCAAAAAGTTGTGAAATTTGCGCCAGCACAGCATTTGGATCCAGAA 780
QY 979 CTGCGTGTATCGCATTTGTGCGGATGAGTAAAGTTCTGCGCTCCATTGGTTACCGGSC 1038
Db 781 CTGCGTGTATCGCATTTGTGCGGATGAGTAAAGTTCTGCGCTCCATTGGTTACCGGSC 840
QY 1039 GCGGGAACCGTGGAAATCTTTGGTTCGATGAAAGGGCAACACACGCTTTTCATCGAAATGAAC 1098
Db 841 GCGGGAACCGTGGAAATCTTTGGTTCGATGAAAGGGCAACACACGCTTTTCATCGAAATGAAC 900
QY 1099 CCACGTATCCAGTTGAGCACACCGTACTGAAGAAAGTCAACCGAGGTGGACCTGCTGAAG 1158
Db 901 CCACGTATCCAGTTGAGCACACCGTACTGAAGAAAGTCAACCGAGGTGGACCTGCTGAAG 960
QY 1159 GCGCAGATGCGCTTGGCTGCTGTGCAACCTTGAAGGAATGGGTCTGACCCCAAGATAAG 1218
Db 961 GCGCAGATGCGCTTGGCTGCTGTGCAACCTTGAAGGAATGGGTCTGACCCCAAGATAAG 1020
QY 1219 ATCAAGACCCACGGTGCAGCACTGCACTGCGGATCACCAGGAAGATCCAAACACCGC 1278
Db 1021 ATCAAGACCCACGGTGCAGCACTGCACTGCGGATCACCAGGAAGATCCAAACACCGC 1080
QY 1279 TTCCGCCACAGATACCGGAATATCACCGGCTACCGCTCACCAGGCGGAGCTGGCGTTCTG 1338
Db 1081 TTCCGCCACAGATACCGGAATATCACCGGCTACCGCTCACCAGGCGGAGCTGGCGTTCTG 1140
QY 1339 CTTGACGGTGCAGCTCAGCTCGGTGGGAAATCAACCGCACTTTGACTCCATGCTGGTG 1398
Db 1141 CTTGACGGTGCAGCTCAGCTCGGTGGGAAATCAACCGCACTTTGACTCCATGCTGGTG 1200
QY 1399 AAAATGACCTGCCGTGTTCCGACTTTGAAACTGCTGTTGCTGTCACAGCGCGCTTG 1458
Db 1201 AAAATGACCTGCCGTGTTCCGACTTTGAAACTGCTGTTGCTGTCACAGCGCGCTTG 1260
QY 1459 GCTGAGTTACCGTGTCTGGTGTGCAACCAACATTTGGTTTCTGCGTGGCTGCTGCGG 1518

Db 1261 GCTGAGTTTACCGTGTCTGGTGTGCAACCAACATGGTTTCTTGGGTGGTGTGCTGCGG 1320
Qy 1519 GAAGAGGACTTCACTTCCAAAGCGCATCGCCACGGATTTCATTGCGGATCACCCGACCTC 1578
Db 1321 GAAGAGGACTTCACTTCCAAAGCGCATCGCCACGGATTTCATTGCGGATCACCCGACCTC 1380
Qy 1579 CTTGAGGCTCCACCTGCTGATGATGAGCAGGAGCGCATCCTGGATTACTTGGCAGATGC 1638
Db 1381 CTTGAGGCTCCACCTGCTGATGATGAGCAGGAGCGCATCCTGGATTACTTGGCAGATGC 1440
Qy 1639 ACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGTCCCTATCGATAAGCTG 1698
Db 1441 ACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGTCCCTATCGATAAGCTG 1500
Qy 1699 CTTAAACATCAAGGATCTGCGACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGC 1758
Db 1501 CTTAAACATCAAGGATCTGCGACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGC 1560
Qy 1759 CCAGCCGCGTTTGTCTCGTGATCTCCGTGAGCAGGACGCACCTGGCAGTTACTGATACCACC 1818
Db 1561 CCAGCCGCGTTTGTCTCGTGATCTCCGTGAGCAGGACGCACCTGGCAGTTACTGATACCACC 1620
Qy 1819 TTCCGCGATGCACACCGCTTTTGTCTTGGATCCCGAGTCCGCTCATTCGCACTGAAGCCT 1878
Db 1621 TTCCGCGATGCACACCGCTTTTGTCTTGGACCCGAGTCCGCTCATTCGCACTGAAGCCT 1680
Qy 1879 GCGGCAGAGGCGCTGCAAGACTGACTCCTGAGCTTTTGTCCGTGGAGCGCTGGGCGGC 1938
Db 1681 GCGGCAGAGGCGCTGCAAGACTGACTCCTGAGCTTTTGTCCGTGGAGCGCTGGGCGGC 1740
Qy 1939 GCGACCTACGATGTGCGGATCGGTTTCTCTTTGAGGATCCGTGGGACAGGCTCGACGAG 1998
Db 1741 GCGACCTACGATGTGCGGATCGGTTTCTCTTTGAGGATCCGTGGGACAGGCTCGACGAG 1800
Qy 1999 CTGCGGAGGCGGATGCCGAATGTAAACATTTCAGATGCTGCTTCCGCGCGCAACACCGTG 2058
Db 1801 CTGCGGAGGCGGATGCCGAATGTAAACATTTCAGATGCTGCTTCCGCGCGCAACACCGTG 1860
Qy 2059 GGATACACCCCGTACCCAGACTCCGTCTGCGCGCGGTTTGTAAAGGAGTCCAGCTCC 2118
Db 1861 GGATACACCCCGTACCCAGACTCCGTCTGCGCGCGGTTTGTAAAGGAGTCCAGCTCC 1920
Qy 2119 GGCGTGGACATCTTCCGCACTTTCGACGCGCTTAAACGACGTCTCCAGATCGTCCAGCA 2178
Db 1921 GGCGTGGACATCTTCCGCACTTTCGACGCGCTTAAACGACGTCTCCAGATCGTCCAGCA 1980
Qy 2179 ATCGACGAGTCTCTGGAGACCAACACCGCGGTAGCCGAGTGGCTATGGCTTATTCTGGT 2238
Db 1981 ATCGACGAGTCTCTGGAGACCAACACCGCGGTAGCCGAGTGGCTATGGCTTATTCTGGT 2040
Qy 2239 GATCTCTGATCCAAATGAAAAGCTCTACACCCCTGGATTACTACCTTAAAGATGGCAGAG 2298
Db 2041 GATCTCTGATCCAAATGAAAAGCTCTACACCCCTGGATTACTACCTTAAAGATGGCAGAG 2100
Qy 2299 GAGATCGTCAAGTCTGGCGTCAATCTTGGCCATTAAAGGATATGGCTGGTCTGCTTCGC 2358
Db 2101 GAGATCGTCAAGTCTGGCGTCAATCTTGGCCATTAAAGGATATGGCTGGTCTGCTTCGC 2160
Qy 2359 CCAGTGGCGGTAAACCAAGTGGTCAACCGCATGCGCGGTGAATTTCGATCTGCGAGTGCAC 2418
Db 2161 CCAGTGGCGGTAAACCAAGTGGTCAACCGCATGCGCGGTGAATTTCGATCTGCGAGTGCAC 2220
Qy 2419 GTGCACACCCACGACACTGCGGTTGGCCAGCTGGCAACCTACTTTGCTGCAAGCTCAAGCT 2478
Db 2221 GTGCACACCCACGACACTGCGGTTGGCCAGCTGGCAACCTACTTTGCTGCAAGCTCAAGCT 2280
Qy 2479 GGTGCAGATGCTGTTGACCGGTGCTTCCGCAACCTGCTGGCACCACCTCCAGCCATCC 2538
Db 2281 GGTGCAGATGCTGTTGACCGGTGCTTCCGCAACCTGCTGGCACCACCTCCAGCCATCC 2340
Qy 2539 CTGCTGCGCATGTTGCTGCAATTCCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAG 2598
Db 2341 CTGCTGCGCATGTTGCTGCAATTCCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAG 2400

RESULT 8
ABK52832
ID ABK52832 standard; DNA; 3474 BP.

Qy 2599 GCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGGCGGACTGTACTCTGCCATTTGAG 2658
Db 2401 GCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGGCGGACTGTACTCTGCCATTTGAG 2460
Qy 2659 TCTGGAAACCCAGGCCCAACCGGTGCGCTCTACCGCCACGAAATCCAGCGGACAGTTG 2718
Db 2461 TCTGGAAACCCAGGCCCAACCGGTGCGCTCTACCGCCACGAAATCCAGCGGACAGTTG 2520
Qy 2719 TCCAACTGCGTGCAAGGCCACCGCACTGGGCTTTCGGATCGTTTCGAACTCATCGAA 2778
Db 2521 TCCAACTGCGTGCAAGGCCACCGCACTGGGCTTTCGGATCGTTTCGAACTCATCGAA 2580
Qy 2779 GACAACTACGACGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCAACCCCATCTCC 2838
Db 2581 GACAACTACGACGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCAACCCCATCTCC 2640
Qy 2839 AAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGGGTGTGGATCCAGCAGACTTT 2898
Db 2641 AAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGGGTGTGGATCCAGCAGACTTT 2700
Qy 2899 GGTGCCGATCCACAAAAGTACGACATCCAGACTCTGTCTATCGCGTTCCTGCGCGGCGAG 2958
Db 2701 GGTGCCGATCCACAAAAGTACGACATCCAGACTCTGTCTATCGCGTTCCTGCGCGGCGAG 2760
Qy 2959 CTTGGTAAACCTCCAGGTGGCTGGCCAGAGCCACTGGCCACCCGCGCACTGGAAAGGCCGC 3018
Db 2761 CTTGGTAAACCTCCAGGTGGCTGGCCAGAGCCACTGGCCACCCGCGCACTGGAAAGGCCGC 2820
Qy 3019 TCCGAAGCAAGGCACCTCTGACGGAAAGTTCTCTGAGGAAGAGCAGGCGCACTTCGACGCT 3078
Db 2821 TCCGAAGCAAGGCACCTCTGACGGAAAGTTCTCTGAGGAAGAGCAGGCGCACTTCGACGCT 2880
Qy 3079 GATGATTCGAAGGAACGTGCGCAATAGCCTCAACCGCTGCTGTTCCGGAAGCCAAACCGAA 3138
Db 2881 GATGATTCGAAGGAACGTGCGCAATAGCCTCAACCGCTGCTGTTCCGGAAGCCAAACCGAA 2940
Qy 3139 GAGTTCCTCGAGCACCGTCCCGCTTCGGCAACACCTCTGCGTGGATGATCGTGAATTC 3198
Db 2941 GAGTTCCTCGAGCACCGTCCCGCTTCGGCAACACCTCTGCGTGGATGATCGTGAATTC 3000
Qy 3199 TTCTACGGCCTGGTCAAGGCCGCGAGACTTTTGAATCCGCTGCCAGATGTGCGCACCCCA 3258
Db 3001 TTCTACGGCCTGGTCAAGGCCGCGAGACTTTTGAATCCGCTGCCAGATGTGCGCACCCCA 3060
Qy 3259 CTGCTTGTTCGCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTG 3318
Db 3061 CTGCTTGTTCGCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTG 3120
Qy 3319 GCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCTGACCGCTCCGTTGAGTCTGTC 3378
Db 3121 GCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCTGACCGCTCCGTTGAGTCTGTC 3180
Qy 3379 ACCGCAACCGCAGAAAAGSCAGATTCTCTCCAACAAGGGCCATGTTGCTGCACCATTCGCT 3438
Db 3181 ACCGCAACCGCAGAAAAGSCAGATTCTCTCCAACAAGGGCCATGTTGCTGCACCATTCGCT 3240
Qy 3439 GGTGTTGTCAACCGTGAATGCTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGAGTCCGCA 3498
Db 3241 GGTGTTGTCAACCGTGAATGCTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGAGTCCGCA 3300
Qy 3499 ATCATCGAGGCTATGAAGATGAAGCAACAATCACTGCTTCTGTTGACGGCAAAATCGAT 3558
Db 3301 ATCATCGAGGCTATGAAGATGAAGCAACAATCACTGCTTCTGTTGACGGCAAAATCGAT 3360
Qy 3559 CGGTTGTGTTTCTGCTGCAACGAAGGTGGAAGGTGGGCGACTTGATCGTCTGCTTCC 3618
Db 3361 CGGTTGTGTTTCTGCTGCAACGAAGGTGGAAGGTGGGCGACTTGATCGTCTGCTTCC 3420

XX AC ABK52832;
XX DT 27-AUG-2002 (first entry)
XX DE Corynebacterium glutamicum feedback-resistant pyruvate carboxylase gene.
XX KW Feedback-resistant; pyruvate carboxylase enzyme; gene; ds;
XX KW aspartic acid feedback inhibition resistant.
XX OS Corynebacterium glutamicum.
XX XX
XX FH Key Location/Qualifiers
XX FT 1. .3474
XX FT /*tag= a
XX FT /product= "Corynebacterium glutamicum feedback-resistant
XX FT pyruvate carboxylase enzyme"
XX FT /transl_except= (pos:1. .3; aa:Met)
XX XX
XX PN W0200231158-A2.
XX XX
XX PD 18-APR-2002.
XX XX
XX PF 12-OCT-2001; 2001WO-US031893.
XX XX
XX PR 13-OCT-2000; 2000US-0239913P.
XX XX
XX PA (ARCH) ARCHER-DANIELS MIDLAND CO.
XX XX
XX PI Hanke PD;
XX XX
XX DR WPI; 2002-463267/49.
XX DR P-PSDB; AAU98050.
XX XX
XX PT Novel mutated, feedback resistant pyruvate carboxylase enzyme
XX PT polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine,
XX PT L-glycine, L-glutamic acid, L-proline and L-methionine and L-isoleucine.
XX XX
XX PS Claim 3; Fig 1; 42pp; English.
XX XX
XX CC The present invention relates to a new mutated, feedback-resistant
XX CC pyruvate carboxylase enzyme. The invention is useful for producing an
XX CC amino acid (e.g. L-lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by
XX CC culturing a host cell in a suitable media and separating the amino acid
XX CC from the medium. The vector of the invention is useful for replacement of
XX CC a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate
XX CC carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic
XX CC copy of the wild-type pyruvate carboxylase gene with a selectable marker
XX CC gene through homologous recombination to form a first recombinant
XX CC strain, and replacing the selectable marker gene in the first recombinant
XX CC strain, with feedback resistant pyruvate carboxylase gene through
XX CC homologous recombination to form a second recombinant strain, where the
XX CC homologous recombination in the above steps, occurs between the host cell
XX CC and the vector. The feedback-resistant pyruvate carboxylase enzyme is
XX CC resistant to feedback inhibition from aspartic acid. The present nucleic
XX CC acid sequence encodes the feedback-resistant pyruvate carboxylase enzyme
XX CC of the invention
XX SQ Sequence 3474 BP; 749 A; 1013 C; 950 G; 762 T; 0 U; 0 Other;
Query Match 93.9%; Score 3398.8; DB 6; Length 3474;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 3427; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 148 GTGACTGTATCACCCCTGGCGGTCTCTTGTGAAAGGAATAATACTCTAGTGTGACT 207
Db 1 GTGACTGTATCACCCCTGGCGGTCTCTTGTGAAAGGAATAATACTCTAGTGTGACT 60
QY 208 CACACATCTTCAACGCTTCCAGCATTTCAAAAAGATCTTGGTAGCAACCGCGGGAATC 267
Db 61 CACACATCTTCAACGCTTCCAGCATTTCAAAAAGATCTTGGTAGCAACCGCGGGAATC 120
QY 268 GCGGTCCGTGCTTCCGTGAGCAGCACTCGAAACCGGTGCGAGCCAGGTAGTATTTACCCC 327

Db 121 GCGGTCCGTGCTTCCGTGAGCACTCGAAACCGGTGAGCCACGGTAGCTATTACCCC 180
QY 328 CGTGAAGATCGGGGATCATCCACCGCTCTTTTGTCTTCTGAAGCTGTCCGCATGGTACC 387
Db 181 CGTGAAGATCGGGGATCATCCACCGCTCTTTTGTCTTCTGAAGCTGTCCGCATGGTACT 240
QY 388 GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATATATCGGTGAGCTGAGTAA 447
Db 241 GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATATATCGGTGAGCTGAGTAA 300
QY 448 GTTAAAGCAGATGCCATTACCCGGGATACGGCTTCTGTCTGAAATATGCCAGCTTGCC 507
Db 301 GTTAAAGCAGATGCTATTTACCCGGGATATGGCTTCTGTCTGAAATATGCCAGCTTGCC 360
QY 508 CGCAGTGTGCGGAAACCGGCAATTACTTTTATTGGCCCAACCCAGAGTTCTTGATCTC 567
Db 361 CGCAGTGTGCGGAAACCGGCAATTACTTTTATTGGCCCAACCCAGAGTTCTTGATCTC 420
QY 568 ACCGTGATAAGTCTCGCGCGGTAAACCGCCGCGAAGAGGCTGGTCTGCCAGTTTGGCG 627
Db 421 ACCGTGATAAGTCTCGGTGCGGTAAACCGCCGCGAAGAGGCTGGTCTGCCAGTTTGGCG 480
QY 628 GAATCCACCCCGAGCAAAACATCGATGAGATCGTTAAAGCGCTGAAGGCCAGACTTAC 687
Db 481 GAATCCACCCCGAGCAAAACATCGATGAGATCGTTAAAGCGCTGAAGGCCAGACTTAC 540
QY 688 CCCATCTTTGTGAAGGCGATGTCGCGGTGGTGGCGGCGCGGTATGCGTTTGTGCTTCA 747
Db 541 CCCATCTTTGTGAAGGCGATGTCGCGGTGGTGGCGGCGCGGTATGCGTTTGTGCTTCA 600
QY 748 CCTGATGAGCTTCGCAAAATTAGCAACAGAAAGCATCTCGTGAAGCTGAAGCGGCTTCGGC 807
Db 601 CCTGATGAGCTTCGCAAAATTGCAACAGAAAGCATCTCGTGAAGCTGAAGCGGCTTCGGC 660
QY 808 GATGGCGCGTATATGTCGAAGCTGCTGTGATTAACCTCTCAGCATATTGAAGTGCAGATC 867
Db 661 GACGGTTCGGTATATGTCGAAGCTGCTGTGATTAACCCCGAGCAGTGAAGTGCAGATC 720
QY 868 CTTGGCGATCACACTGGAGAAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT 927
Db 721 CTTGGCGATCGCACTGGAGAAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT 780
QY 928 CGTCAACCAAAAGTTGTGCAAAATTGCGCCAGCACAGCAATTTGGATCCAGAACTGCGTAT 987
Db 781 CGTCAACCAAAAGTTGTGCAAAATTGCGCCAGCACAGCAATTTGGATCCAGAACTGCGTAT 840
QY 988 CGCATTTGTGCGGATGCAATAAGTTCTGCCGCTCCATTTGGTTACAGGGCGCGGAAAC 1047
Db 841 CGCATTTGTGCGGATGCAATAAGTTCTGCCGCTCCATTTGGTTACAGGGCGCGGAAAC 900
QY 1048 GTGGAATTTCTTGGTTCGATGAAAGGGCAACACCGTCTTTCATCGAAATGAACCCACGTATC 1107
Db 901 GTGGAATTTCTTGGTTCGATGAAAGGGCAACACCGTCTTTCATCGAAATGAACCCACGTATC 960
QY 1108 CAGGTTGAGCACACCGGTGACTGAAGAAAGTCAACCGAGGTGGACCTGGTGAAGGCGCAGATG 1167
Db 961 CAGGTTGAGCACACCGGTGACTGAAGAAAGTCAACCGAGGTGGACCTGGTGAAGGCGCAGATG 1020
QY 1168 CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCCAAGATAAGATCAAGACC 1227
Db 1021 CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCCAAGATAAGATCAAGACC 1080
QY 1228 CACGGTGCAGCACTGCAGTGCAGCATCACCGGATCACCGAGAGATCCAAACCAACGGCTTCCGCCCA 1287
Db 1081 CACGGTGCAGCACTGCAGTGCAGCATCACCGGATCACCGAGAGATCCAAACCAACGGCTTCCGCCCA 1140
QY 1288 GATACCGGAATATCACCGGTACCGCTCACCGAGGAGTGGCGTTCGTCTTGACGGT 1347
Db 1141 GATACCGGAATATCACCGGTACCGCTCACCGAGGAGTGGCGTTCGTCTTGACGGT 1200
QY 1348 GCAGCTCAGTCTGGTGGGAAATCAACCGGCACACTTTGACTCCATGCTGTTGAAATGACC 1407

Db 1201 GCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTTGACTCCATGCTGGTGAAATGACC 1260
Qy 1408 TGCCGTGGTTCGACTTTGAAACTGCTGTGCTCGTGACAGCGCGCGTGGCTGAGTTC 1467
Db 1261 TGCCGTGGTTCGACTTTGAAACTGCTGTGCTCGTGACAGCGCGCGTGGCTGAGTTC 1320
Qy 1468 ACCGTGTCTGGTGTGCAACCAACATTGGTTTCTTGCGTGGCTGCTGCGGGAAGAGAC 1527
Db 1321 ACCGTGTCTGGTGTGCAACCAACATTGGTTTCTTGCGTGGCTGCTGCGGGAAGAGAC 1380
Qy 1528 TTCACTTCCAAGCGCATCGCCACCGGATTCAATGCCGATCACCCGCACCTCCTTCAGGCT 1587
Db 1381 TTCACTTCCAAGCGCATCGCCACCGGATTATCGGCGATCACCCACACCTCCTTCAGGCT 1440
Qy 1588 CCACCTGTGTGATGAGCAGGGAAGGATCTCTGGATTACTTGGCAGATGTACCGTGAAC 1647
Db 1441 CCACCTGCGGATGATGAGCAGGGAAGGATCTCTGGATTACTTGGCAGATGTACCGTGAAC 1500
Qy 1648 AAGCCTCATGTGTGCGTCCAAAGGATGTGACGCTCCTATCGATAAGCTGCCTAACATC 1707
Db 1501 AAGCCTCATGTGTGCGTCCAAAGGATGTGACGACCAATCGATAAGCTGCCCAACATC 1560
Qy 1708 AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCTGAAGCAGCTTGGCCCCAGCCGG 1767
Db 1561 AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCTGAAGCAGCTTGGCCCCAGCCGG 1620
Qy 1768 TTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACTTCCGCGAT 1827
Db 1621 TTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACTTCCGCGAT 1680
Qy 1828 GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCANTCGCACTGAAGCCTGCGGCAGAG 1887
Db 1681 GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCANTCGCACTGAAGCCTGCGGCAGAG 1740
Qy 1888 GCCGTGCGAAAGTGAATCCTGAGCTTTGTCGTTGGAGGCTGCGGCGCGCGCAGCTTAC 1947
Db 1741 GCCGTGCGAAAGTGAATCCTGAGCTTTGTCGTTGGAGGCTGCGGCGCGCGCAGCTTAC 1800
Qy 1948 GATGTGGCGATGCGTTTCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 2007
Db 1801 GATGTGGCGATGCGTTTCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 1860
Qy 2008 GCGATGCCGAATGTAAACATTCAGATGCTGCTCGCGGCCGCAACACCGTGGGATACACC 2067
Db 1861 GCGATGCCGAATGTAAACATTCAGATGCTGCTCGCGGCCGCAACACCGTGGGATACACC 1920
Qy 2068 CCGTACCCAGACTCCGTCTGCGCGCGTTTGTAAAGAAAGCTGCCAGCTCCGCGGTGGAC 2127
Db 1921 CCGTACCCAGACTCCGTCTGCGCGCGTTTGTAAAGAAAGCTGCCAGCTCCGCGGTGGAC 1980
Qy 2128 ATCTTCCGCATCTCGACGCGCTTAACGACGCTCTCCAGATGCGTCCAGCAATCGACGCA 2187
Db 1981 ATCTTCCGCATCTCGACGCGCTTAACGACGCTCTCCAGATGCGTCCAGCAATCGACGCA 2040
Qy 2188 GTCTTGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTTGGTGATCTCTCT 2247
Db 2041 GTCTTGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTTGGTGATCTCTCT 2100
Qy 2248 GATCCAAATGAAAGCTCTACACCCCTGGATTACTACCTAAAGATGCGAGGAGATCGTC 2307
Db 2101 GATCCAAATGAAAGCTCTACACCCCTGGATTACTACCTAAAGATGCGAGGAGATCGTC 2160
Qy 2308 AAGTCTGGCGCTCAGATCTTGGCCATTAAAGGATATGGCTGCTGCTCGCCCGAGCTGCG 2367
Db 2161 AAGTCTGGCGCTCAGATCTTGGCCATTAAAGGATATGGCTGCTGCTCGCCCGAGCTGCG 2220
Qy 2368 GTAAACCAAGCTGGTCAACCGCACTGCGCGGTGAATTCGATCTGCCAGTGCACGCAACC 2427
Db 2221 GTAAACCAAGCTGGTCAACCGCACTGCGCGGTGAATTCGATCTGCCAGTGCACGCAACC 2280
Qy 2428 CACGACACTGCGGTGCCAGCTGGCAACCTACTTTGCTGACGCTCAAGCTGGTGCAGAT 2487
Db 2281 CACGACACTGCGGTGCCAGCTGGCTACTACTTTGCTGACGCTCAAGCTGGTGCAGAT 2340

Qy 2488 GCTGTTGACGGTGTCTCCGCACCACTGTCTGGCACCACTCCCGAGCCATCCCTGTCTGCC 2547
Db 2341 GCTGTTGACGGTGTCTCCGCACCACTGTCTGGCACCACTCCCGAGCCATCCCTGTCTGCC 2400
Qy 2548 ATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCCGTTTGAGCCTCGAGGCTGTTTCT 2607
Db 2401 ATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCCGTTTGAGCCTCGAGGCTGTTTCT 2460
Qy 2608 GACCTCGAGCGCTACTGGGAAGCAGTGGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC 2667
Db 2461 GACCTCGAGCGCTACTGGGAAGCAGTGGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC 2520
Qy 2668 CCAGGCCCCAACCGGTGCGGTCTACCGCCACGAAATCCAGGCGGACAGTTGTCCAAACCTG 2727
Db 2521 CCAGGCCCCAACCGGTGCGGTCTACCGCCACGAAATCCAGGCGGACAGTTGTCCAAACCTG 2580
Qy 2728 CGTGACAGGCGCACCGCACTGGGCTTGGGATCGTTTCGAACTCATCGAAGACAATAC 2787
Db 2581 CGTGACAGGCGCACCGCACTGGGCTTGGGATCGTTTCGAACTCATCGAAGACAATAC 2640
Qy 2788 GCAGCCGTTAATGAGATGCTGGGACGCGCCAAACCAAGGTCAACCCATCCTCCAAGGTTGTT 2847
Db 2641 GCAGCCGTTAATGAGATGCTGGGACGCGCCAAACCAAGGTCAACCCATCCTCCAAGGTTGTT 2700
Qy 2848 GCGGACCTCGCACTCCACCTCGTTGGTGGGATGGATCCAGCAGACTTTGCTGCCGAT 2907
Db 2701 GCGGACCTCGCACTCCACCTCGTTGGTGGGATGGATCCAGCAGACTTTGCTGCCGAT 2760
Qy 2908 CCACAAAAGTACGACATCCAGACTCTGTCTCATCGGCTTCTGCGGCGGAGCTTGGTAAC 2967
Db 2761 CCACAAAAGTACGACATCCAGACTCTGTCTCATCGGCTTCTGCGGCGGAGCTTGGTAAC 2820
Qy 2968 CCTCCAGGTGGCTGGCCAGAGCCACTGCGCACCCGCGCACTGGAAGCCGCTCCGAAGGC 3027
Db 2821 CCTCCAGGTGGCTGGCCAGAGCCACTGCGCACCCGCGCACTGGAAGCCGCTCCGAAGGC 2880
Qy 3028 AAGGCACCTCTGACGGAAGTTCTCTGAGGAAGAGCAGGCGCACTCGACGCTGATATCC 3087
Db 2881 AAGGCACCTCTGACGGAAGTTCTCTGAGGAAGAGCAGGCGCACTCGACGCTGATATCC 2940
Qy 3088 AAGGAACGTGCGCAATAGCCTCAACCGCCTGCTTCCCGAAGCCAAACCGAAGAGTTCCCTC 3147
Db 2941 AAGGAACGTGCGCAATAGCCTCAACCGCCTGCTTCCCGAAGCCAAACCGAAGAGTTCCCTC 3000
Qy 3148 GAGCACCGTCCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATCTTCTACGGC 3207
Db 3001 GAGCACCGTCCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATCTTCTACGGC 3060
Qy 3208 CTGGTCGAAGGCGCGAGACTTTGATCCGCTGCCAGATGTGCGCAACCCCACTGCTTGT 3267
Db 3061 CTGGTCGAAGGCGCGAGACTTTGATCCGCTGCCAGATGTGCGCAACCCCACTGCTTGT 3120
Qy 3268 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAAACGTC 3327
Db 3121 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAAACGTC 3180
Qy 3328 AACGGCCAGATCCGCCCAATCGGTGCGTGACCGCTCCGTTGAGTCTGTCAACCGCAACC 3387
Db 3181 AACGGCCAGATCCGCCCAATCGGTGCGTGACCGCTCCGTTGAGTCTGTCAACCGCAACC 3240
Qy 3388 GCAGAAAAGGAGATTCCTCCAAACAAAGGGCATGTTGTGCAACCAATCGCTGGTGTGTC 3447
Db 3241 GCAGAAAAGGAGATTCCTCCAAACAAAGGGCATGTTGTGCAACCAATCGCTGGTGTGTC 3300
Qy 3448 ACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGAGTGCAGATCATCGAG 3507
Db 3301 ACTGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGAGTGCAGTGCAGATCATCGAG 3360
Qy 3508 GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTGACGGCAAAATCGATCGCTTGTG 3567
Db 3361 GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTGACGGCAAGATTGAACGCTTGTG 3420

QY 3568 GTTCTGCTGCAACGAAGGTGGAAGTGGCGACTTGATCGTCGTCGTTTCCCTAA 3621
Db |||||
3421 GTTCTGCTGCAACGAAGGTGGAAGTGGCGACTTGATCGTCGTCGTTTCCCTAA 3474
|||
RESULT 9
AAF87437
ID AAF87437 standard; DNA; 4013 BP.
XX AC AAF87437;
XX DT 09-JUL-2001 (first entry)
XX DE Corynebacterium thermoaminogenes pc nucleotide sequence.
XX KW Corynebacterium; thermophilic; amino acid biosynthesis; enzyme;
KW thermotolerant; aceA; accBC; dtsR1; pfk; scrB; gluABCD; pdhA; pc;
KW ppc; acn; icd; lpd; odhA; ds.
XX OS Corynebacterium thermoaminogenes.
XX FH Key Location/Qualifiers
FT CDS 319..3738
FT /*tag= a
FT /product= "pc protein"
XX PN W0200125447-A1.
XX PD 12-APR-2001.
XX PF 04-OCT-2000; 2000WO-JP006913.
XX PR 04-OCT-1999; 99JP-00282716.
XX PR 01-NOV-1999; 99JP-00311147.
XX PR 21-APR-2000; 2000JP-00120687.
XX PA (AJIN) AJINOMOTO CO INC.
XX PI Hirano S, Nonaka G, Matsuzaki Y, Akiyoshi N, Nakamura K;
PI Kimura E, Osumi T, Matsui K, Kawahara Y, Kurahashi O, Nakamatsu T;
PI Sugimoto S;
XX WPI; 2001-300170/31.
DR P-PSDB; AAB83180.
XX
PT Proteins and their DNA useful for microbial production of L-amino acids.
XX
PS Claim 34; Page 126-132; 215pp; Japanese.
XX
CC The present sequence is provided in a specification relating to genes
CC encoding thermophilic amino acid biosynthesis system enzymes of the
CC thermotolerant bacterium Corynebacterium thermoaminogenes. The novel
CC proteins retain at least 30% isocitrate ligase activity after heating at
CC 50oC for 5 minutes. DNA fragments encoding the enzymes were isolated from
CC a Corynebacterium thermoaminogenes chromosomal DNA plasmid library by
CC PCR. The DNA may be used for developing strains of amino acid producing
XX microorganisms
SQ Sequence 4013 BP; 735 A; 1376 C; 1234 G; 668 T; 0 U; 0 Other;
Query Match 63.0%; Score 2279.6; DB 5; Length 4013;
Best Local Similarity 77.7%; Pred. No. 0;
Matches 2808; Conservative 0; Mismatches 799; Indels 9; Gaps 4;
QY 7 GGGGTTAGATCCTGGGGGTTTATTTCATTCACCTTTGGCTTGAAGTCGTGCAGGTCAGGG 66
Db |||||
129 GGGGTCTCGGCGGGGGGCATTCCTTTACGGCAAGGTGGTGAATTCGCGAGGTCACTC 188
QY 67 GAGTGTGCCGAAACATTGAGAGGAAACAAACACCGATGTTTATTGGGGGATCGG 126
Db |||||
189 CCGGCGGGGTAGAGAACGGAGCGAAACGGAAAGCAATACGTGGTTCCTCCGACTGG 248
QY 127 GGGTTACGATACTAGGACGCAGTGTCTATCACCCTT--GGCGGTCTCTTTGTTGAAAG 184
|||

Db 249 CCGTTACGATGTTCTGAAG-AGTGACTGCCATCACCCAAACAGGCTGGTCTCGTGAAG 307
QY |||||
185 GAATAATTACTCTAGTGTGCACTCACACATCTTCAACGCTTCCAGCATTCRAAAAGATCT 244
Db |||||
308 GAACAAAAAATGTGGTTACAACA--ACACCTCCACGCTCCCGCGGTTCAAAAAGATCC 364
QY |||||
245 TGGTAGCAAAACCGCGCGGAATTCGGTCCGTCCTTCCGTGCGAGCATTCGAAACCGGTG 304
Db |||||
365 TGGTGGCAACCGAGGTGAATTCGGTGGAGCATTCGGCGCGCTACGAGACCGGGG 424
QY |||||
305 CAGCCACGGTAGCTATTATCCCGCGTGAAGATCGGGGATCATTCACCGCTCTTTTCTT 364
Db |||||
425 CCGCAACCGTGGCCATCTACCCCGGGAGGACCGTGGTCTCTCCACCGCTCTCGCCT 484
QY |||||
365 CTGAAGCTGTCCGCTTGTACCGAAGGCTCACCCAGTCAAGGCGTACCTGGACATCGATG 424
Db |||||
485 CCGAGCGGTGAGGATCGGAACCGAGGGCTCACCCCTCAAGGCGTACCTCGATATTGATG 544
QY |||||
425 AAATTATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTACCCGGGATACGGCTTCC 484
Db |||||
545 AGATCATCAACGCCGCCAAGAGGTGAAGCGGACGCGGTCTACCCGGGGTATGGTTTCC 604
QY |||||
485 TGTCTGAAAAATGCCAGCTTCCCGCGAGTGTGCGGAAAAACGGCATTTATTATTGGCC 544
Db |||||
605 TTTCGAAAAATGCCAGCTCCCGGTGAATGCGCGGAGAACCGCATTTACCTTCATCGGTC 664
QY |||||
545 CAACCCAGAGGTTCTTGTATCTACCGGTGATAAGTCTCGCGCGGTAAACCGCGCGAAGA 604
Db |||||
665 CCACCCCGAGGTGCTCGACTCACGGGCGACAAGTCCAAGGCTGTGTCCGCCGCGAAGA 724
QY |||||
605 AGGCTGCTGCCAGTTTGGCGGAATCCACCCCGAGCAAAAAACATCGATGAGATCGTTA 664
Db |||||
725 AGGCGGGCTGCCGTGCTGGCGGAATCCACCCCGAGCACCGACATCGATGAGATCGTCA 784
QY |||||
665 AAAGCGCTGAAGCCAGACTTACCCCATCTTTGTGAAGGCGAGTTGCCGGTGGTGGCGGAC 724
Db |||||
785 AGAGTCCGAGGGGCGAGACTACCCGATCTTCGTCAAGGCGCTCGCAGGTGGTGGCGGGC 844
QY |||||
725 GCGGTATGCGTTTTTGTGTTTACCTGATGAGCTTCGCAAAATTAGCAACAGAAAGCATCTC 784
Db |||||
845 GTGGTATGCGGTTCTGTCGAGAAGCCCGAGGACCTGCTGAGCTGGCCAGGGAGGCTCCC 904
QY |||||
785 GTGAAGCTGAAGCGGCTTTTCGGCGATGGCGGTTATATGTGAAACGCTGTGTGATTAACC 844
Db |||||
905 GCGAGCGGAGGCGCGCTTTTCGGTACGGATCCGCTCTACGTCGAACGGGCGCTGATCAAAC 964
QY |||||
845 CTCAGCATATTGAAGTGCAGATCCTTTGGCGATCACACTGGAGAAGTTGTACACCTTTATG 904
Db |||||
965 CCCAGCATCGAGGTGAGATCCTCGGTGATCACACCGCGATGTATCCACCTGTATG 1024
QY |||||
905 AACGTGACTGCTCACTGCAGCTGCTCACCAAAAAGTTGTGCGAAATTGCGCCAGCACAGC 964
Db |||||
1025 AACGCGACTGTTCCCTGCGAGCGCGGCCACCAAGAGTGTGAGATCGCACCTGCCAGC 1084
QY |||||
965 ATTTGGATCCAGAACTGCGTATGCGCATTTGTGCGGATGCGAGTAAAGTTCTGCCGTCCA 1024
Db |||||
1085 ACCTCGACCCGGAGCTGCGGACCGCATCTGTGCCGATGCGGTGAAGTTCTGCAATCCA 1144
QY |||||
1025 TTGTTACCGGCGCGGGAACCGTGAATTTCTTGGTCGATGAAAAGGGCAACCCAGTCT 1084
Db |||||
1145 TCGGATACCGAGGCGCGGACCGTGGAGTTCTCTGTCGACGAGGCGGGCAACCCAGTCT 1204
QY |||||
1085 TCATCGAAATGAACCCACGTTATCCAGGTTGAGCACACCGTGAAGTGAAGAAGTCAACCGAGG 1144
Db |||||
1205 TCATTGAGATGAACCCCGCATCCAGGTGGAACACACCGTGAACCGAGGAGGTCACTCCG 1264
QY |||||
1145 TGGACCTGGTGAAGGCGCAGATGCGCTTGGTGTGTTGCGAACCTTGAAGGAATTGGGTC 1204
Db |||||
1265 TCGACCTGGTCAAGGCGCAGATGACCTGGCCCGCGGTGCCACCTGAAGGAAGTGGGCG 1324
QY |||||
1205 TGACCCCAAGATAAGATCAAGACCCACCGGTGCAGCTGCGAGTCCCGCATCACCCAGGAAG 1264
|||

Db 1325 TGACCCAGGACAAGATCACACCCACCGGTGCGGCCCTGCAGTGCCTGCATCACCACGGAGG 1384
Qy 1265 ATCCAAACAACGGCTTCGCGCCAGATACCGGAACACTATCACCGCGTACCGTACACGAGCG 1324
Db 1385 ACCCGTCCAAACAATTCGGGCCGACACCGGTGTGATCACCGCTACCGTCCCGGGTG 1444
Qy 1325 GAGCTGGCGTTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGGCACACTTTG 1384
Db 1445 GTGCGGTGTGCGTCTCGACGGCGCAGCCAGCTCGCGGGCGAGATCACCGGCACATTTCG 1504
Qy 1385 ACTCCATGCTGGTGAATATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTGCTCGTG 1444
Db 1505 ATTCCATGCTGGTCAAGATGACCTGCCCGGTTCCGATTTTCGAGACCGCGGTGTCCTCGAG 1564
Qy 1445 CACAGCGCGCTTGGCTGAGTTTACCGTGTCTGCTGTGTTGCAACCAACATTTGTTCTTGC 1504
Db 1565 CCCAGCGCCCTGGCGGAGTTCAACGTCTCCGCGTGGCCACCAACATCGGCTTCTTGC 1624
Qy 1505 GTGCGTTGCTGCGGGAAGAGACTTCACTTCCAAAGCGCATCGCCACCGGATTCATTGCCG 1564
Db 1625 GTGCGTGTGCGGAGGAAGACTTCAACCAAGAGCGCATCGACACCGGCTTCATCGGCT 1684
Qy 1565 ATCACCCGCACCTCCTTCAAGCTCCACCTGCTGATGATGAGCAGGAGCGCATCCTGGATT 1624
Db 1685 CCCACGACACTGCTCCAGGCCCCACCGGCCGACGATGAGCAGGGCGGATCCTTGAAT 1744
Qy 1625 ACTTGGCAGATGTCAACGTGAACAAGCCTCATGTGTGCTGCTCCAAAGGATGTTGCAGCTC 1684
Db 1745 AACTGGCGGATGTCAACGTGAACAACCCCAACCGTGAACGCCC--CGAGACAGCCCCGTC 1801
Qy 1685 CTATCGATAAGCTGCCATAACATCAAGGATCTGCCACTGCCACCGGTTCCCGTGACCGCC 1744
Db 1802 CGATAGAGAAGCTGCCAGGTGGAGAAACATCCCGCTGCCACCGGCTCCCGCGACCGCC 1861
Qy 1745 TGAAGCAGCTTGGCCCGAGCGGTTTTCGCGCGATCTGCGCGAACAGGATGCCCTGGCCG 1804
Db 1862 TGAAGCAGCTCGGCCCGAGGGTTTTCGCGCGATCTGCGCGAACAGGATGCCCTGGCCG 1921
Qy 1805 TTAAGTATACCACTTCCCGGATGACACACAGTCTTTGCTTGCACCGCGGTTCCCGTGACCT 1864
Db 1922 TCACCGACACCACTTCCCGGATGCCACCAAGTCTTCTTGGCCACCGCGGTGCGCTCCT 1981
Qy 1865 TCGCACTGAAGCCTTCCGCGAGAGCGCGTCCGAAAGTGAATCCTGAGCTTTTGTCCGTGG 1924
Db 1982 TCGCGCTGACCCCGCGCGCGCGCGTCCGAAAGTCAACCCCGAGCTGCTGCTGCGTGG 2041
Qy 1925 AGGCTGGGGCGCGCGACCTACGATGTGGCGATGCGTTTCTCTTTGAGGATCCGTGGG 1984
Db 2042 AGGCTGGGGCGGTGCCACCTACGACGTGGCCATGCGCTTCTCTTCGAGGATCCGTGGG 2101
Qy 1985 ACAGGCTCGACGAGCTGCGGAGGCGGATGCCGAATGTAAACATTCAGATGCTGCTCGCG 2044
Db 2102 CACGCTGGATGAGCTGCGTGAGGCGGATGCCGAATGTGAACATCCAGATGCTGCTGCGTG 2161
Qy 2045 GCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCGCGCGTTTGTAAAG 2104
Db 2162 GTCGCAACACCGTCCGGGTACACCCCGTACCCCGATTCCGTTGTCGCGCGGTTTGTGCGAG 2221
Qy 2105 AAGCTGCCAGCTCCGGCGTGGACATCTTCCGCACTCTGACGCGCTTAACGACGTCTCCC 2164
Db 2222 AGGCGCCCAAGTCCGGTGTGGACATCTTCCGCACTCTGACGCGCTCAACGACATCTCCC 2281
Qy 2165 AGATGGTCCAGCAATCGACGAGTCTCTGATCCAAATGAAAGCTCTACACCCCTGGATTACTCC 2224
Db 2282 AGATGGCCCGGCCATCGACGCGCTCCTGGAGACCGSCACCAAGTGTTCGCGAGGTGCGCA 2341
Qy 2225 TGGCTTATCTGGTGTCTCTGTGATCCAAATGAAAGCTCTACACCCCTGGATTACTACC 2284
Db 2342 TGGCTACTCCGGTACCTGTCCAATCCGGGGAGAGCTCTACACCCCTGGACTACTACC 2401
Qy 2285 TAAAGATGCGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAAGGATATGG 2344
Db 2402 TGAACCTGGCCGAGCAGATCGTGCAGTCCGGTGCACACATCTCTGGCCATCCTGGCCATCAGGACATGG 2461

Qy 2345 CTGGTCTGCTTCCGCCAGCTGCGGTAAACCAAGTGGTCAACCGCACTGCGCGTGAATTTCG 2404
Db 2462 CCGGCTGTGCGCGCGCGCGCGCCAAATGGTCAACCGCTTGCCTGCGCGTGAATTTCG 2521
Qy 2405 ATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTG 2464
Db 2522 ACCTGCCCGTGCATGTCCACACCCACGACACCGCGCGGTGAGTGGCCACCTACTACTGG 2581
Qy 2465 CTGCAGTCAAGCTGGTGCAGATGCTGTTGACGGTGTTCGCAACCACTGTTCGGCACCA 2524
Db 2582 CCGCGCCAAACGCGCGGCGCGATGCCGTGCAGCCGCTCCGACACCCCTGTCCGGTACCA 2641
Qy 2525 CTTCCAGCCATCCCTGTCTGCCATTGTTGTCGANTCGCGCACACCCGTGCGGATACCG 2584
Db 2642 CTTCCAGCCCGTGCATGTCCGCTCTGTTGCGCGTTCGCGCACACCCGACGCGACACCG 2701
Qy 2585 GTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCGGTACTGGGAAGCAGTGGCGGACTGT 2644
Db 2702 GCCTCAACCTGCAGGCGCTCTCCGACCTGGAACCGTACTGGAGGCGGTCCGCGGACTGT 2761
Qy 2645 ACCTGCCATTGAGTCTGGAACCCAGGCCCAACCGGTCGCTCTACCGCACGAAATCC 2704
Db 2762 ACCTGCCGTTTGAATCCGCGCACCCCGGGCCCGACGCGTTCACCGCACGAGATCC 2821
Qy 2705 CAGCGGACAGTTGTCCAACTCGTGCAGCAGGCCACCGCACTGGGCTTGGGATCGTT 2764
Db 2822 CCGCGGTGAGTGTCCAACTCGTGCAGCGCCAGCGCTGCACTGGGTCTGCGCGACCGCT 2881
Qy 2765 TCGAACTCATCGAAAGACAACACTACGAGCGCTTAATAGATGCTGGGACGCCCAACCAAGG 2824
Db 2882 TCGAGCTCATCGAGGACTACTACGCGCGCTCAACGAGATGCTGGTCTGCGCACCAAGG 2941
Qy 2825 TCACCCCATCTCCAAAGTGTGCGGACCTCGCACTCCACCTCGTTGTTGGGTGGTGG 2884
Db 2942 TCACCCCGTCTCCAAAGTGTGCGTGACCTCGCACTGCACCTCGTGGTGGCGTGTGA 3001
Qy 2885 ATCAGCAGACTTTGCTGCCGATCCACAAAGTACGACATCCAGACTCTGTCTATCGCT 2944
Db 3002 GCCCGAGGATTTCCGCGCGGATCCGCAAGTACGACATCCCGATTTCGTTCTATCGCT 3061
Qy 2945 TCCTCGCGCGGAGCTTGTGTAACCTCCAGGTGGTGGCCAGAGCCACTGCGCACCCCGG 3004
Db 3062 TCCTCGCGCGGAACTGGGTACCTCCCGTGGTGGCCGGAACCGCTGCGCACCCCGTG 3121
Qy 3005 CACTGGAAGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCTTGAGGAAGAGCAGG 3064
Db 3122 CACTGAGGGTCTCTCCAGGGTAAGCCCGCTGGCGGAGATCCCGCCGCGAGGAGCAGG 3181
Qy 3065 CGCACTCGACGCTGATGATTCGAAGGAACGTGCAATAGCCTCAACCCGCTGTGTTC 3124
Db 3182 CCCACTGGATTCCGATGATTCGCGGAGCGTCCGCGCACCTCAACCCGCTGTGTTC 3241
Qy 3125 CGAAGCCAAACCGAAGATTCTCTGAGCACCGTCCGCGCTTCGGCAACACCTCTGCGCTGG 3184
Db 3242 CGAAGCCGACCGAGGAGTTCTTTCGAGCACCGTCCGCGCTTCGGCAACACCTCCGCTGG 3301
Qy 3185 ATGATCGTGAATTCTTTCAGGCTTGGTTCGAAGGCGCGGAGACTTTGATCCGCTGCCAG 3244
Db 3302 ATGACCGCGAGTTCTTTCAGGCTTGAAGGAGGAGCTGAGGAGCTGATCCGACTGACCG 3361
Qy 3245 ATGTCGCAACCCCACTGCTTTCGCTGCTGATGCGATCTCTGAGCCAGACGATAGGGTA 3304
Db 3362 GTGTCTCACCCCGATGTTGTTGCTGCGCTGATGCGGTGTCGGAACCGGATGACAAAGGCA 3421
Qy 3305 TGGCAATGTTGTGGCCAAAGTCAACGGCCAGATCCGCCCCAATGCGTGTGCGTGACCGCT 3364
Db 3422 TGGCAACGTTGTTGTTCAAGTCAACGGCCAGATCCGCCCCGATCAAGTGTGCGGACCGTT 3481
Qy 3365 CCGTTGAGTCTGTACCGCAACCGCAGAAAGGAGATTCCTCCAAAGGGCCATGTTG 3424
Db 3482 CCGTGGAGTCCGTACCGCCACCGCGGAGGAGGCGGATGCCACCAAGGGCCATGTCG 3541

QY 3425 CTGCACCATTCGCTGGTGTGTTCACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTG 3484
Db |||||
QY 3485 GAGATGCAGTCGCAATCATCGAGGCTATGAAGATGAAGCAACAATCACTGCTTCTGTTG 3544
Db GCGACCGCTGGCCATCATTTAGGCCATGAAGATGGAGGCCACCATCACCGCGCTGTGCG 3661
QY 3545 ACGGCAAAATCGATCGCGTGTGTTCTCTGCTGCAACGAAGGTGGAAGTGGCGACTTGA 3604
Db |||||
QY 3605 TCGTCTGCTGTTTCTTA 3620
Db TCGTGTGCTGTTCTTA 3737

RESULT 10
ACA29831
ID ACA29831 standard; DNA; 3423 BP.
XX
AC ACA29831;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #11488.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Corynebacterium diphtheriae.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU25961.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 17701; 1766pp; English.
XX

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 3423 BP; 773 A; 1058 C; 912 G; 680 T; 0 U; 0 Other;

Query Match 53.2%; Score 1927.4; DB 7; Length 3423;
Best Local Similarity 73.4%; Pred. No. 0;
Matches 2494; Conservative 0; Mismatches 896; Indels 9; Gaps 2;

QY 213 ATCTCAACGCTTCCAGCAATCAAAAAGATCTTGGTAGCAACCCGCGGCAATCGCGGT 272
Db |||||
QY 273 CCGTGCTTCCGTGCGACACTCGAAACCGGTGCGCACGGTAGCTATTATCCCGGTGA 332
Db GCGAGCTTTTCTGTGCGACCTTTGAAACCGGTGCTGCCACGGTAGCTGTCTACCGAACGA 146
QY 333 AGATCGGGGATCATTCACCGCTCTTTTGTCTTGAAGCTGTCCGATTTGGTACCGAAGG 392
Db |||||
QY 147 AGACCGTAATTCATTCACCGATCGTTTGCCTCTGAAGCTGTCTCATTTGGTGAGGCGG 206
QY 393 CTCACGAGTCAAGCGGTACTCGACATCGATGAATATTCGGTGCAGCTAAAAAGTTAA 452
Db ATCTGCGTCAAAGCGTACTTCGATATCGACGAATCATCCGTGCTGTAAACAACGGG 266
QY 453 AGCAGATGCCATTACCCGGGATACGGCTTCTGTCTGAAAATGCCAGCTTCCCGCGGA 512
Db TGCCGACGCAATTTACCCAGGTACGGCTTCTTCCGAAAACGCCAGCTTGTCTCGTGA 326
QY 513 GTGTGCGGAAAACGGCAATTACTTTTATTTGGCCCAACCCACAGAGGTTCTTGATCTCACCGG 572
Db GTGCGTGA AAAACGGCATAACCTTTATCGTCCACCTCCATCATGCTGAGCTTACCGG 386
QY 573 TGATAAGTCTCGCGGTAAACCGCGCGGAAGAGGCTGTGCTGCCAGTTTGGCGGGAATC 632
Db TGATAAAGCAGCTGCTGTTTACCGCAGCACGCGAGGAGGTTTGGCCACGCTGACTGAGAC 446
QY 633 CACCCCGAGCAAAAACATCGATGAGATCGTTAAAAAGCGCTGAAGGCCAGACTTACCCCAT 692
Db AGAAGCAACAGACGATCCAAAGAGCTCGCAGAGCTGACCAAGGGGCAGACTACCCGCT 506
QY 693 CTTTGTGAAGCGAGTTGCCGTTGTTGGCGGACGCGGTATGCGTTTGTGTTTCACTGA 752
Db ATTGCTCAAAGCCGTTGCCGTTGTTGGTGGCGCGCATGCGTTTGTGACGCCCCCGA 566
QY 753 TGAGCTTCGCAAAATTAGCAACAGAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGG 812
Db AAACCTAGAAAAGCTAGCAGCAGAGAGCTCCCGTGAGGCGGCTGAGCATTCGGCGGATGG 626
QY 813 CGCGGTATATGTCGAACGCTGCTGTGATTAAACCTTCAGCATATTGAAGTGCAGATCCTTGG 872
Db CCGAGTCTACGCGAGCGTGCAGTAATCAATCCTCAGCATATTGAGGTCCAGATCCTTGG 686
QY 873 CGATCACACTGGAGAAGTTGTACACCTTTATGAACGCTGACTGCTCACTGCAGCGTGTCA 932
Db TGACTCCGCTGSCAACATCATCCACCTGTACGAGCGGTGATTGCTGCTGAGCGTGTGCGCA 746
QY 933 CCAAAAAGTTGCGAAATTGCGCCGACGACAGCATTTGGATCCAGAACTGCGTGATCGCAT 992
Db |||||

Db 747 CCAAAAGGTCGTAGATCGCCCCAGCACAGCACTGGCGCCCGGACTACGGAAAGAT 806
QY 993 TTGTGCGGATGCAGTAAAGTTCTGCGCTCCATTGGTTACCAGSGCGGGAACCGTGGA 1052
Db 807 TTGTGCAGACGCAGTCGGTTTGCAACGCCACATCGGTTACCAAGGTGCAGGCACGGTCGA 866
QY 1053 ATTCTTGGTCGATGAAAGGCAACCAACGCTCTTCATCGAAATGAACCCACGATCCAGGT 1112
Db 867 GTTCCTAGTCGATGAGGAAGGCAACCAACGCTCTTCATCGAGATGAACCCCTCGTATCCAGGT 926
QY 1113 TGAGCACACCGTGACTGAAGAAAGTCAACCGAGGTGACCTGGTGAAGSGCGAGATGCGCTT 1172
Db 927 CGAACACACCGTGACCGGAAGAGGTCAACCAAGTCGACTTGGTGAAGTCCAGATCATGAT 986
QY 1173 GGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCCAAGATAAGATCAAGACCCACCG 1232
Db 987 CGCCTCCGGTGGCACTCGAAGATCTCGGTCTGGCCCAAGAACATCCACACCGAAGG 1046
QY 1233 TGCAGCACTGCAGTGCAGCATCACCAACCGGAAGATCCAAACCAACGGCTTCGCCCCAGATAC 1292
Db 1047 CGCTGCCCTGCAGTGCCTGATTACTACTGAAGACCCCAACCAACGGTTTCGCTCCTGACAC 1106
QY 1293 CGGAACATATCACCCGCTACCGCTCACCAAGCGGAGCTGGCGTTTCGTTCTGACGGTGCAGC 1352
Db 1107 CGGAACGATTACCGCTTATCGTTCCCGAGGTGGCGCAGGTGTTCTGTTCTGACGGTGTGC 1166
QY 1353 TCAGCTCGGTGGCGAATCACCGGCACACATTTGACTCCATGCTGGTGAATGACCTGCCG 1412
Db 1167 CATGCTCGGTGGTGAGATCACCCCGAATTTTCGACTCCATGCTGGTCAAGATGACCTGCCG 1226
QY 1413 TGGTTCCGACTTTGAACTGCTGTTGCTCGTGACAGCGCGCGTTGGCTGAGTTACCGGT 1472
Db 1227 TGGTCCGATTTTGGCCACCGCAGTCGCTCGCGCTCAGCGTGCACTCGCAGAATTCGTTGT 1286
QY 1473 GTCTGGTGTGCAACCAACATTTGGTTTCTTGGTGGCGTTGCTGCGGGAAGAGACTTCAC 1532
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QY 1593 TGCTGATGATGAGCAGGAGCGCATCCTGGATTACTTGGCAGATGTACCGTGAACAAGCC 1652
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QY 1653 TCATGGTGTGCTGCCAAAGGATGTTGCAGCTCCTATCGATAAGCTGCCTTAACATCAAGGA 1712
Db 1467 TCATGGTCTACGCCCA---GCCGTGATCAACCCGGTGAAGAAAGTCCCCAGCAGAGATCAA 1523
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Db 1704 CGCAAGCTCACCCAGAGTGTCTCTGTAGAAGCATGGGGTGGTGTACCTATGACGT 1763
QY 1953 GCGATGCGTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGGAGGCGAT 2012
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QY 2013 GCCGAATGTAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACCCCGTA 2072
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QY 2253 AAATGAAAAGCTCTACACCTCTGATTAACCTAAAGATGGCAGAGGAGATCGTCAAGTC 2312
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PR 27-AUG-1999; 99DE-01040765.
PR 31-AUG-1999; 99US-0151572P.
PR 03-SEP-1999; 99DE-01042076.
PR 03-SEP-1999; 99DE-01042079.
PR 03-SEP-1999; 99DE-01042086.
PR 03-SEP-1999; 99DE-01042087.
PR 03-SEP-1999; 99DE-01042088.
PR 03-SEP-1999; 99DE-01042095.
PR 03-SEP-1999; 99DE-01042123.
PR 03-SEP-1999; 99DE-01042125.
XX (BADI) BASF AG.
XX
XX Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX WPI; 2001-061975/07.
DR P-PSDB; AAB79303.
XX
PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
PT metabolism and oxidative phosphorylation protein for production or
PT modulation of production of fine chemicals e.g. amino acids,
PT carbohydrates or enzymes.
XX
PS Claim 3; Page 321-323; 1246pp; English.
XX
CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
CC to AAB 79633 which are involved in carbon metabolism and energy
CC production. The C. glutamicum SMP gene can be used in vectors (II) for
CC expression in host cells and production or modulation of production of
CC fine chemicals, such as, an organic acid, a proteinogenic or
CC nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
CC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,
CC a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III)
CC encoded by them are used for diagnosing the presence or activity of
CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
CC containing them are used to map genomes of organisms related to C.
CC glutamicum, identify and localise C. glutamicum sequences of interest, in
CC evolutionary studies, in determining SMP protein regions required for
CC function, in modulating SMP protein activity, in modulating the
CC metabolism of sugars, and in modulating high-energy molecule production
CC in a cell (i.e. ATP, NADPH)
XX
SQ Sequence 1406 BP; 325 A; 381 C; 385 G; 315 T; 0 U; 0 Other;

Query Match 38.5%; Score 1395; DB 4; Length 1406;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1406; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 361 GCTTCTGAAGCTGTCGCGATTGGTACCGAAGGCTCACCGATCAAGGCGTACCTGGACATC 420
Db |||||
QY 421 GATGAAATTATCGGTGCAGCTAAAGTTAAAGCAGATGCCATTACCCGGGATACGGC 480
Db |||||
QY 61 GATGAAATTATCGGTGCAGCTAAAGTTAAAGCAGATGCCATTACCCGGGATACGGC 120
QY 481 TTCCTGTCTGAAATGCCCCAGCTTGCCCGGAGTGTGCGGAAACCGGCATTACTTTTATT 540
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QY 121 TTCCTGTCTGAAATGCCCCAGCTTGCCCGGAGTGTGCGGAAACCGGCATTACTTTTATT 180
QY 541 GGCCCAACCCCGAGAGTTCTTGATCTACCGGTGATAAGTCTCGCGGGTAAACCGCCGGC 600
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QY 181 GGCCCAACCCCGAGAGTTCTTGATCTACCGGTGATAAGTCTCGCGGGTAAACCGCCGGC 240
QY 601 AAGAAGGCTGGTCTGCCAGTTTGGCGGAAATCCACCCGAGCAAAACATCGATGATC 660
Db |||||
QY 241 AAGAAGGCTGGTCTGCCAGTTTGGCGGAAATCCACCCGAGCAAAACATCGATGATC 300
QY 661 GTTAAAGCGCTGAAGCCAGACTTACCCCATCTTTGTGAAGGCGTTCGCGGTGGTGGC 720
Db |||||
QY 301 GTTAAAGCGCTGAAGCCAGACTTACCCCATCTTTGTGAAGGCGTTCGCGGTGGTGGC 360
Db |||||

QY 721 GGACGGGTATGCGTTTGTGCTTACCTGATGAGCTTCGAAATTAGCAACAGAAGCA 780
Db |||||
QY 361 GGACGGGTATGCGTTTGTGCTTACCTGATGAGCTTCGAAATTAGCAACAGAAGCA 420
Db |||||
QY 781 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGGATATATGTGAAACGTGCTGATT 840
Db |||||
QY 421 TCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGGATATATGTGAAACGTGCTGATT 480
QY 841 AACCTTCAGCATATTGAAGTCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
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QY 481 AACCTTCAGCATATTGAAGTCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 540
QY 901 TATGAACGTGACTGCTCAGTCAGCGTCTGTCACCAAAAAGTTGTGAAAATTGGCGCAGCA 960
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Db |||||

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QY 2098 GTTAAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCACTTTCGACGCGCTTAACGAC 2157
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QY 2218 GTGGCTATGGCTATTCTGGTGTATCTCTGTATCCAAATGAAGCTCTACACCCCTGGAT 2277
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QY	3418	CATGTTGCTGCACCAATTGCTGTTGTACCGTGACTGTTGCTGAAGGTGATGAGGTC	3477
Db	19863	CACATCGCCCGGCCAATTGCCGAGTCGTACGGTCGGGTGTGCGTCCGCGAGCGGGTC	19804
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Db	19683	GACCTGTTGGTGGTGGTGAAGTGA	19660

Search completed: March 23, 2004, 18:35:43
Job time : 1318 secs

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 17:20:33 ; Search time 237 Seconds
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Perfect score: 3621
Sequence: 1 tggggggggttagatcctg.....tgatcgtcgttcctaa 3621

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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C 3	1294.4	35.7	4403765	3	US-09-103-840A-2
C 4	1294.4	35.7	4411529	3	US-09-103-840A-1
5	1249.6	34.5	32155	4	US-08-311-731A-1
6	509.2	14.1	3492	4	US-09-134-000C-2302
7	486.2	13.4	3465	4	US-09-134-001C-591
8	479.8	13.3	5030	4	US-08-956-171E-324
9	476.2	13.2	2922	4	US-09-107-532A-1156
10	313.4	8.7	1362	4	US-09-543-681A-1699
11	313	8.6	1362	1	US-07-956-700B-5
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13	313	8.6	1362	1	US-08-485-607-5
14	313	8.6	1362	2	US-08-475-879-5
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C 28	298.6	8.2	3065	4	US-09-433-043B-1	Sequence 1, Appli
C 29	297.4	8.2	2907	4	US-09-252-991A-2354	Sequence 2354, Ap
30	288.6	8.0	1511	4	US-09-634-238-58	Sequence 58, Appl
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C 37	251.6	6.9	119211	4	US-09-596-002-40	Sequence 40, Appl
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ALIGNMENTS

RESULT 1

US-09-220-081-1

; Sequence 1, Application US/09220081

; Patent No. 6171833

; GENERAL INFORMATION:

; APPLICANT: Sinskey, Anthony J.

; APPLICANT: Lessard, Philip A.

; APPLICANT: Willis, Laura B.

; APPLICANT: Stephanopoulos, Gregory

; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum

; FILE REFERENCE: 1533.0790000

; CURRENT APPLICATION NUMBER: US/09/220,081

; CURRENT FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 3621

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (199)..(3621)

US-09-220-081-1

Query Match 100.0%; Score 3621; DB 3; Length 3621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 35.7%; Score 1294.4; DB 3; Length 4403765;
Best Local Similarity 62.0%; Pred. No. 0;
Matches 2099; Conservative 0; Mismatches 1276; Indels 9; Gaps 3;
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DB	3315628	TCCGTGGAGTGTGGGCGGTGCGACTTACGATGTGGCGCTGCGCTTCTCAAGGAGGAT	3315569
QY	1978	CCGTGGGACAGGCTCGACGAGCTGCGCGAGCGCATGCCGAATGTAACAATTCAGATGCTG	2037
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QY	2758	GATCGTTTCGAACTCATCGAAGACAACACTACGAGCCGTTAATGAGATGCTGGGACGCCA	2817
Db	3314788	GATCGATTGGAAGAGATCGAAGAGGCTACGCGGGCGCGACCGAGTGTGGGAGGCTG	3314729
QY	2818	ACCAAGTCAACCCATCCTCCAAGTGTGTGGCGACCTCGCACTCCACCTCGTTGGTGGC	2877
Db	3314728	GTTAAGGTACGCCAACGTCCAAGTGGTGGCGATCTGGCGTGGCACTGGTGGCGGCC	3314669
QY	2878	GGTGTGGATCCAGCAGACTTTGCTGCCGATCCACAAAAGTACGACATCCAGACTCTGTC	2937
Db	3314668	GGTGTGAGTGCAGACGAATTTCGCTCCGATCCAGGCGGATTTGGCATCCCGGAATCGGTA	3314609
QY	2938	ATCGCGTTCTGCGCGCGAGCTTGGTAAACCTCCAGGTGGCTGGCCAGAGCCACTGGCG	2997
Db	3314608	CTCGGATTTCTGCGGGCGAGCTGGTGTATCCGCCCGCGGTGGCCCGAACCGCTGGC	3314549
QY	2998	ACCCGCGCACTGGAAGCCGCTCCGGAAGCAAGGCACCTTGACGGAAGTTCTTGAGGAA	3057
Db	3314548	ACTGCGGCTGCGCGGTGCGGGGCGCGCAGGCCCACT--GCGCAATTGGCGGCGGAC	3314492
QY	3058	GAGCAGCGCACCTCGACGCTGATGATTCCAAGGAACGTGCAATAGCTCAACCGCTG	3117
Db	3314491	GACGAGATTGCCCTATCGTCGGTCGGAGCCAAG--CGTCAGGCCACCTGAACAGGCTG	3314435
QY	3118	CTGTTCCCGAAGCCAAACCGAAGATTCTCGAGCACCGTCCGCGCTTCGGCAACACCTCT	3177
Db	3314434	TTATTTCCAGTCCAAACAAAGGAATTCATGAGCACCGGGAAGCTACGGCGACACGCTG	3314375
QY	3178	GCGCTGGATGATCGTGAATTCTTCTACGCGCTGGTGAAGCGCGGAGACTTTGATCCGC	3237
Db	3314374	CAATTGTCGGCCAACCAAGTTCTTCTATGTTCTGCGCCAAGTGAAGAGCATCGGGTGAAG	3314315
QY	3238	CTGCCAGATGTGCGCACCCCACTGCTTGTTCGCTGGATGCGATCTCTGAGCCAGACGAT	3297

Db 3314314 CTG---GAGCGTGGGTGGAGCTGTTGATCGGGCTGGAGGCCATTTCGAAACCCGACGAA 3314258
QY 3298 AAGGTATGCGCAATGTTGTGGCCAAAGTCAACGGCCAGATCCGCCCAATGCGTGTGCGT 3357
Db 3314257 CGCGCATGCGAAACGGTGATGTGATCCTCAACGGGAGCTGCGGCCGTTGCTAGTGC 3314198
QY 3358 GACCGTCCGTTGAGTCTGTACCGCAACCGCAGAAAGGAGAGATTCTTCCAAACAAGGCG 3417
Db 3314197 GACCGCAGCATGCCAGTGCCGTTCCGGCCCGCAGAGAGGCCGACCGCGCAATCCCGGA 3314138
QY 3418 CATGTTGCTGCACCATTCGCTGGTGTGTGTCACCGTGACTGTTGCTGAAGGTGATGAGTTC 3477
Db 3314137 CACATCGCCGCGCCATTGTCGGAGTGTGTCACGGTCCGGGTGTGCGTCGGCGAGCGGGTC 3314078
QY 3478 AAGCTGGAGATGAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCT 3537
Db 3314077 GCGCGCGGCAAAACCATCGCCACCATCGAGGCGATGAAGATGGAAGCCCGCATCACCGCC 3314018
QY 3538 TCTGTTGACGCAAAATCGATCGCGTGTGTTCTGCTGCAACGAAGGTGGAAGGTGCG 3597
Db 3314017 CCGGTTGCCGACCGTGGAGCGGTGGCGGTGTGCGGACACCGCCAGGTGGAGGGCGGA 3313958
QY 3598 GACTTGATCGTGTGCTTTCCTAA 3621
Db 3313957 GACCTGTTGGTGGTGAGCTGA 3313934

RESULT 4

US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-2007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 35.7%; Score 1294.4; DB 3; Length 4411529;
Best Local Similarity 62.0%; Pred. No. 0;
Matches 2099; Conservative 0; Mismatches 1276; Indels 9; Gaps 3;
QY 238 AAGATCTTGGTAGCAACCGCGGGAATCCGGTCCGTGCTTCCGTGCAGCACTCGAA 297
Db 3323034 AAGGTGCTCGTCGCCAATCGCGGGAGATCGCGATCCGGGCTTTCGTGCCGCTACGAA 3322975
QY 298 ACCGGTGCAGCCACGGTAGCTATTTACCCCGTGAAGATCGGGGATCATTCACCGCTCT 357
Db 3322974 CTGGCGTTCGGAACCGTGGCCGTTTATCCGTACGAGGACCGCAATTCGAGCACCGTCTC 3322915
QY 358 TTTGCTTCTGAAGTGTCCCGCATTTGATCCGAAGGCTCACCGATCAAGCGGTACCTGGAC 417
Db 3322914 AAGCGGACGAGTCTTACAGATCGGCGACATCGGTCAACCGGTGCATACCTGTGC 3322855
QY 418 ATCGATGAAATATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTTACCCGGGATAC 477
Db 3322854 GTCGACGAGATCGTCGCGACGGCCCGTCCGGGCGGTGCCGACGCTATCTACCTGGCTAC 3322795
QY 478 GGCTTCTGTCTGAATAATGCCAGCTTGCCTCCGAGTGTGCGGAAACGGCATTAATTTT 537
Db 3322794 GGGTTCTATCGGAGATCCGGATCTGGCTGCGGCATCGCGGCGGCGGCATCAGCTTC 3322735

QY 538 ATTGGCCCAACCCAGAGGTTCTTGTATCTCACCGGTGATAAGTCTCGCGCGGTAAACCGCC 597
Db 3322734 GTCGGTCCAGCGCCGAAGTCTTGAAGTGGTGGGATAAGTCTCGCGCCATCGCGGCG 3322675
QY 598 GCGAAGAAGGCTGCTGCCAGTTTGGCGGAATCCACCCGAGCAAAAACATCGATGAG 657
Db 3322674 GCCCGGAAGCCGGCTTGCCCGTGTGATGTCTCGGCGCGTTCGGCTCGGTTCGACGAA 3322615
QY 658 ATCGTTAAAAAGCGCTGAAGCGCAGACTTACCCCATCTTTGTGAAGGCAGTTTCCGGTGT 717
Db 3322614 CTGCTGCGGTTGCGGCGCGCATCCGTTTCCGTTGTTCTCAAGGCAGTTTCCCGTGGC 3322555
QY 718 GCGGACGCGGTATCGGTTTGTGCTTACCTGATGAGCTTCGCAATTAGCAACAGAA 777
Db 3322554 GGGGCGCGGTATCGTCTGTGCGCGATATCGCGCGCTTCGGAGGCGATCGAAGCC 3322495
QY 778 GCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGGCTATATGTGAAACGTGCTGTG 837
Db 3322494 GCCAGCGGGAAGCCGAGTCGCGCTTCGGGACCCGACCGTCTATCTCGAGCAGGCGAGT 3322435
QY 838 ATTAACCTCAGCATATTGAAGTGCAGATCTTGGCGATCACACTGGAGAAGTTGTACAC 897
Db 3322434 ATCAATCCAGCCACATCGAGGTGCAGATTCTGGCGGACAACTTCGGCGACGTGATCCAT 3322375
QY 898 CTTTATGAACGTGACTGCTCACTGCAGCGCTCGTCACCAAAAAGTTGTGAAATTCGCGCA 957
Db 3322374 CTCTATGAGCGTGA CTGCA GTGTGAGCGTGCCTATCAGAGGTTCATCGAGCTGCGGCC 3322315
QY 958 GCACAGCATTTGGATCCAGAACTGCGTGTGATCGCATTTTGTGCGATGCGATAAGTTCTGC 1017
Db 3322314 GCGCGCACCTGGACCGCGAGTTGCGTTACAAGATGTGCTGATGCGTTCGCTTCGCC 3322255
QY 1018 CGCTCCATTGTTACAGGGCGCGGAAACCGTGGAAATCTTGTGATGAAAGGGCAAC 1077
Db 3322254 CGCCATATCGGTAAGTCAAGTGTGCGTTCAGAGTTCTTGTGACGAGCGAGGGGAG 3322195
QY 1078 CAGCTTTCATCGAAATGAACCCACGTATCCAGTTTGAGCACACCGTGAAGAGTCA 1137
Db 3322194 TATGTCTTCATGAGATGAATCCCGCGGTTCAAGTTGGAGCACACCGTGAACGAGATT 3322135
QY 1138 ACCGAGGTGACCTGGTGAAGGGCGAGATCGCTTGGCTGTGCTGCTGCAACCTTGAAGAA 1197
Db 3322134 ACCGAGTGCACCTGGTGCACGCCAGTGCATTTGCCCGGGAGACGCTCGAACAA 3322075
QY 1198 TTGGTCTGACCCCAAGATAAGATCAAGACCCACGGTGCAGCATGCTGCGTCCGCTACCC 1257
Db 3322074 TTGGGCTGCGGAGGAGACATCGCACCGCATGGCGCGCACTACAGTCCGGATCAC 3322015
QY 1258 ACGAAGATCCAAACACGGCTTCGCCCCAGATACCGGAACCTATCACCGGTACCGCTCA 1317
Db 3322014 ACCGAGGATCCGGCCAAACGGCTTCGCCCGGACACGGGCGGATCAGCGCTTTCGCC 3321955
QY 1318 CCAGGCGAGTGGCGTTCGTCTTGAAGGTGAGTCAAGTGCAGTCAAGTCCGTGCGGAAATCACCGCA 1377
Db 3321954 GCCGCGGTGCCGCTGTCCGCTGGACGGCAGCACCAACCTGGGCGCAGAAATCAGCCCG 3321895
QY 1378 CACTTTGACTCCATGCTGGTGAATAAGTCACTGCGGTGTTCCGACTTTGAACCTGCTTT 1437
Db 3321894 TACTTCGACTCCATGCTGTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3321835
QY 1438 GCTCGTGCACAGCGCGCTTGGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1497
Db 3321834 AGCCGTGCGCGCGGCGATCGCGAGTTCCGGATCCGCGGGGTATCGACGAATATTCGG 3321775
QY 1498 TTCTTGCCTGCTGCTGCGGGAAGAGACTTCACTTCAAGCGCATTCGCCACCGGATTC 1557
Db 3321774 TTCTTGAAGCGGCTGCTGATGACCCGAGTCCGAGCGGCGGTCACCGTCTCTTC 3321715
QY 1558 ATTGCGGATCACCCGACCTCTTCAAGGTTCACCTGTGATGATGAGCAGGACGATC 1617
Db 3321714 ATTGATGAGCGCGCGAGTCTGTGACCCGCGCGCTCGGCCGACCGGCGACCAAGATC 3321655

QY	1618	CTGGATTACTTGGCAGATGTCA	CGGTGAACAAGCCCTCATGGTGTGCGTCCAAAGGATGTT	1677		
DB	3321654	CTTAACTTCCTGGCCGATGTCA	CGGTCAACAACCCCGTATGGCTCGCGTCCGTCAACGATC	3321595		
QY	1678	GCAGTCCCTATCGATAAGCT	GCCTAAACATCAAGGATCTGC	CACTGCCACGCGGTTCCCGT	1737	
DB	3321594	TACCCGGACGACAAGCTG	CCCGATCTTGATCTCGGGCCG	CACACCGGCCGGTCCAAG	3321535	
QY	1738	GACCGCTGAAGCAGCTTGG	CCCAAGCCGCTTTGCTCGTGATCT	CCGTGAGCAGACGCA	1797	
DB	3321534	CAGCGACTAGTCAAGTTGG	GGCCGGAAGGATTTGCTCGTTGGCT	TCGGGAGTCGGCCGCG	3321475	
QY	1798	CTGGCAGTTACTGATACCA	CTTCCGGGATGCACACCACTGCTT	TGCTTGCACCCGAGTC	1857	
DB	3321474	GTCGGGGTCACCGATACCA	CAATTCGGGATGCTCACCAGT	CGTTACTGGTACCCGAGTA	3321415	
QY	1858	CGCTCATTCGCACTGAAG	CCCTGCGGAGAGCCGTCG	CAAAAGCTGACTCCTGAGCTTTG	1917	
DB	3321414	CGCACCGCGACTGTCGG	GGTGGCACCGTATCTCGCGCGG	ACCATGTCGCGCAGTGTG	3321355	
QY	1918	TCCGTGGAGGCTGGGG	CGGCGGACCTACGATGTGG	CGGATGCGTTTCTCTTTGAGGAT	1977	
DB	3321354	TCCGTGGAGTGTGGGG	CGGTGCGACTTACGATGTGG	CGCTTCTCAAGGAGGAT	3321295	
QY	1978	CGGTGGGACAGGCTCGA	CGAGCTGCGCGAGGCGAT	GCCGAATGTAAACATTCAGATGCTG	2037	
DB	3321294	CCCTGGGAACGCTGGCC	ACACTGCGTGCAGCAAT	GCCCCAATATCTGTTGCAGATGCTA	3321235	
QY	2038	CTTCGGGCGCGCAAC	CACCGTGGGATACACCCG	TACCCGTAACCCAGACTCCGTCGCCGCGGCTTT	2097	
DB	3321234	TTGCGGGGCGCGAATAC	CGTGGGCTACACGCCGT	ACCCGCTACCCGGAATCGTGACGTGCGGCGTT	3321175	
QY	2098	GTTAAGGAAGTGGCAG	CTCCGGGTGGACATCTT	CCGCATCTTCGACCGCGCTTAACGAC	2157	
DB	3321174	GTGCAAGAAGCAACAG	CCACCGGTATCGACATCTT	CGTATCTTCGACCGCTCAACAAC	3321115	
QY	2158	GTCTCCAGATGGTCC	CAGCAATCGACGAGTCT	TGGAGACCAACACCGCGGTAGCCGAG	2217	
DB	3321114	ATCGAGTCGATGCTT	CCGGCATCGACGAGTAC	GCGAGTACGGAACAGGTTCTGCGATAGCAGAA	3321055	
QY	2218	GTGGCTATGGCTTATCT	TGGTGATCTCTCTGATCT	CAATGAAAGCTCTACACCCCTGGAT	2277	
DB	3321054	GTCCGATGTGCTACA	CGGCGACCTTACCGAT	CCGGGTGAACAGTGTACACGCTGGAC	3320995	
QY	2278	TACTACCTAAGATG	GCAGAGGAGATCGTCA	AGTCTGGCGTCAATCTTGCCCATTAAG	2337	
DB	3320994	TACTACCTGAAC	TGCTGAGCAGATCGT	GACCGCGCGGCCCATGTGCTGGCGATCAAG	3320935	
QY	2338	GATATGGCTGGTCTG	TCGCCAGCTGCGGTA	ACCAAGCTGGTCACCGCACTGCGCCGT	2397	
DB	3320934	GATATGGCTGACTG	TTGCGCCCGCCGCGCT	CAAGGTTGGTCAGCGCCCTGCGCAGT	3320875	
QY	2398	GAATTCGATCTG	CCAGTCACGTGCACAC	CCCAAGCACTGCGGGTGGCCAGCTGGCAACC	2457	
DB	3320874	CGCTTCGACCTG	CCCCGTTACCTGCA	CACCCAGACACACCGGGTGGCCAGCTCGCCAGC	3320815	
QY	2458	TACTTTGCTGCAG	CTCAAGCTGGTG	CAGATGCTGTTGACCGTGTCTCCGCACCACTGTCT	2517	
DB	3320814	TATGTGGCCGCTT	GGCAGCCGGGCGGAT	GGCGTCGACGGCGCCGCGCGCTGGCG	3320755	
QY	2518	GGCACCACTCC	CAGCATCCCTGTCTG	CCATTGTTGCTGCATTCGGCCACACCCCGTCGC	2577	
DB	3320754	GGAACGACCA	CGCAGCCCGGCTG	AGCTCGATCGTTGCTGCCGTGCCACACCCGAGTAC	3320695	
QY	2578	GATACCGGTTT	TGAGCCTCGAGGCTG	TTTCTGACCTCGAGCCGTACTGGGAAGCAGTGGCG	2637	
DB	3320694	GACACCGGCCT	GTGCGTTTCGGCGGT	GTGCGCTGCTGCCGTGCCACACCCGAGTAC	3320635	
QY	2638	GGACTGTACTG	CCATTTGAGTCTGGA	ACCCAGGCCAAACCGGTTCGGTCTACCGCCAC	2697	
DB	3320634	AAAGTGATG	CGCCGTTTCGAGTCT	GGGTTGCCGGGCCGACGGGGCGGTTTATCACCAC	3320575	
QY	2698	GAAATCCAGG	CGGACAGTTGTCCA	ACCTGCGTGCA	CAGGCCACCGCACTGGGCCCTTGCG	2757

Db	3320574	GAGATTCGGGGCGGCCAACTGTCCAATCTGCGCCAGCAAGCAATTGCTCTTGCTCTGGGA	3320515
QY	2758	GATCGTTTCGAACCTCATCGAAGACAACTACGACGCGTTAATGAGATGCTGGACGCCCA	2817
Db	3320514	GATCGATTGGAAGAGATCGAAGAGGCCCTACGCGGGCGCCGACCGAGTGTGGCAGGCTG	3320455
QY	2818	ACCAAGGTCACCCCATCCTCCAAAGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGGC	2877
Db	3320454	GTTAAGGTCACGCCAAACGTCAAAGGTGGTCGGCGATGCGCTGGCACTGGTCGGCGCC	3320395
QY	2878	GGTGTGGATCCAGCAGACTTTTGCTGCCGATCCACAAAAGTACGACATCCAGACTCTGTC	2937
Db	3320394	GGTGTCAGTGCAGACGAATTGCGCTCCGATCCAGCGGATTTGGCATCCCGGAATCGGTA	3320335
QY	2938	ATCGCGTTCTCGCGGGCGAGCTTGGTAAACCTCCAGGTGGCTGGCCAGAGCCACTGCGC	2997
Db	3320334	CTCGGATTTCTCGGGGCGAGCTGGGTGATCCGCCCGGGGTGGCCCGAACCGTGGC	3320275
QY	2998	ACCCGCGCACTGGAAGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCCTGAGGAA	3057
Db	3320274	ACTGCGCGCTGGCCGTTCGGGGCGCGCCAGGCCCACT--GCGCAATTGGCGCGGAC	3320218
QY	3058	GAGCAGCGCACCTCGACGCTGATGATTCCAAGGAACTCGCAATAGCCTCAACGCGCTG	3117
Db	3320217	GACGAGATTGCCCTATCGTCGGTCGGAGCCAAG--CGTCAGGCCACCTGAAACAGGCTG	3320161
QY	3118	CTGTTCCGAAGCCAAACCGAAGAGTTCTCTGAGCACCGCTCGCGCTTCGGCAACACCTCT	3177
Db	3320160	TTATTTCCAGTCCAAACAAGGAATTCAATGAGCACCCGGAAGCCTACGGCGACACGTCG	3320101
QY	3178	GCGCTGGATGATCGTGAATCTTCTACGGCCTGGTCGAAGCCGCGAGACTTTTGATCCGC	3237
Db	3320100	CAATTGTCGGCCAAACAGTCTCTATGCTCGGCCCAAGGTGAAGAGCATCGGGTGAAG	3320041
QY	3238	CTGCCAGATGTGGCACCCCACTGCTTGTTCGCCTGGATCGCATCTCTGAGCCAGACGAT	3297
Db	3320040	CTG--GAGCGTGGGTGGAGCTGTGATCGGGCTGGAGGCCAATTCGGAACCCGACGAA	3319984
QY	3298	AAGGTAATGCGCAATGTTGTGGCCAACTCAACGGCCAGATCCGCCCAATGCGTGTGCGT	3357
Db	3319983	CGCGCATCGAACGGTGATGTGCACTCTCAACGGGCGAGCTGCGGCCGCTAGTGC	3319924
QY	3358	GACCGTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGCAGATTCTCTCAACAAGGC	3417
Db	3319923	GACCGCAGCATGCCAGTGCCGTTCCGGCCGCCGAGAAGGCCGACCGCGGCAATCCCGGA	3319864
QY	3418	CATGTTGCTGCACCAATTCGTTGTTGTACCGTGATCACCCTGCTGAGGTGATGAGTTC	3477
Db	3319863	CACATCGCCCGGCCAATTTGCCGAGTCCTCACGGTCGGGGTGTCCGTCGGCGAGCGGTC	3319804
QY	3478	AAGGCTGGAGATGCAGTCCCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCT	3537
Db	3319803	GGCGCCGGCCAAACCATCGCCACCATCGAGCGATGAAGATGGAAGCCCCGATCACCGCC	3319744
QY	3538	TCTGTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTGGAAGTGGC	3597
Db	3319743	CCGGTTCGCGGCAACCGTGGAGCGGTGGCGGTGTCCGACACCGCCAGGTGGAGGGCGGA	3319684
QY	3598	GACTTGATCGTCGTTTCTCTAA	3621
Db	3319683	GACCTGTTGGTGGTGGTGGTGA	3319660

RESULT 5
US-08-311-731A-1
; Sequence 1, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID
; TITLE OF INVENTION: RELATING TO
;

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM TUBERCULOSIS
;
US-08-311-731A-1

Query Match 34.5%; Score 1249.6; DB 4; Length 32155;
Best Local Similarity 62.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 1274; Indels 13; Gaps 7;

Qy 238 AAGATCTTGGTAGCAACCGCGCGGAAATCGCGGTCCGTCTTCCGTGCGAGCACTCGAA 297
Db 1574 AAGGTCTCGTCGCCAATCGCGGGAGATCGCGATCCGGCCCTTTCGTGCCGCTACGAA 1633

Qy 298 ACCGGTCAGCCACGGTAGCTATTACCCCGTGAAGATCGGGATCATTTCCACCGCTCT 357
Db 1634 CTGGCGTCGGAACCGTGGCCGTTATCCGTACGAGGACCGCAATTGGCAGACCGTCTC 1693

Qy 358 TTTGCTTCTGAAGCTGTCCGATGGTACCGAAGGCTCACCAGTCAAGGGCTACCTGGAC 417
Db 1694 AAGCGGACGAGTCTTACCAGATCGCGGACATCGGTACCCGGTGCATGCAATACCTGTCG 1753

Qy 418 ATCGATGAAATTATCGGTGCGAGCTAAAGTTAAAGCAGATGCCATTACCCGGGATAC 477
Db 1754 GTCGACGAGATCGTCGCGACCGGCCGTCGGCGGTGCCGACGCTATCTACCCCTGGCTAC 1813

Qy 478 GGCTTCCTGTCTGAAAATGCCAGTTGCCGAGTGTGCGGAAAACGGCAATTACTTTT 537
Db 1814 GGGTTTCTATCGGAGAAATCCGGATCTGGCTGCGGCATGCCGCGCGGGGCATCAGCTTC 1873

Qy 538 ATTGGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAAACCGCC 597
Db 1874 GTCGGTCCAGCGCCGAAAGTGTGAGCTGGGTGGGAATAAGTCTCGCGCCATCGCGCG 1933

Qy 598 GCGAAGAGCGTGGTCTGCCAGTTTGGCGGAATCCACCCGAGCAAAAACATCGATGAG 657
Db 1934 GCCCGGAAGCCGGCTTGCCCGTGTGATGTCCTCGCGCGCTCGGCCTCGGTCCGACGAA 1993

Qy 658 ATCGTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGCTGGT 717
Db 1994 CTGCTGTCCGTTGCGCGCGGATGCCGTTTCCGTTGTTCTGTTCAAGGCAGTTGCCGCTGC 2053

718 GCGGACGCGGTATGCGTTTTTGTGCTTACCTGATGAGCTTCGCAAAATTAGCAACAGAA 777
Db 2054 GGGGCGCGGTATGCGTGTGCGGATATCGCGGCTTCGAGGCGGATCGAAGCC 2113

Qy 778 GCATCTCGTGAAGCTGAAGCGGCTTTCGCGGATGCGCGGTATATGTCGAACGTGCTGTG 837
Db 2114 GCCAGCCGGAAGCGAGTCCGCTTCGCGGACCCGACCGGTCTATCTCGAGCAGGCAAGT 2173

Qy 838 ATTAACCCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGAGAAAGTTGTACAC 897
Db 2174 ATCAATCCACGCCACATCGAGGTGCAGATTCTGGCGGACAACTCGCGACGTGATCCAT 2233

Qy 898 CTTTATGAACGTGACTGCTCACTGCGCGGTGCTGACCAAAAAGTTGTCGAAATTCGCGCA 957
Db 2234 CTCTATGAGCGTCACTGAGTGTGCGCGGTGCGCATCAGAAGGTATCAGACTGGCGGCC 2293

Qy 958 GCACAGCATTTGGATCCAGAACTGCGTGAATGCGCATTTGTGCGGATGAGTAAAGTTCTGC 1017
Db 2294 GCGCGCACCTGGACGCGGAGTTGCGTTACAAGATGTGCTCGATGCGGTGCGCTTCGCC 2353

Qy 1018 CGCTCCATTGTTTACCGAGGCGCGGAAACCGGTGCGCATTTGTGCGATGAAAGGCGAAC 1077
Db 2354 CGCCATATCGGTACAGTGTGCGGCGCACCGGTGAGTTCTGTGACGAGCGGAGGAG 2413

Qy 1078 CACGTCTTCATCGAATGAACCCACGTAATCCAGGTGAGCACACCGTGAAGAAAGTC 1137
Db 2414 TATGTCTTCATCGAGATGAATCCGCGGTTCAGGTGAGCACACCGTGAAGGAGATT 2473

Qy 1138 ACCGAGGTGAGCTGTGTAAGGCGCAGATGCGTTGGTGTGTCGTAACCTTGAAGGAA 1197
Db 2474 ACCGAGTGTGACCTGTGCGCAGCCAGCTGCGCATGCGCGGAGACGCTCGAACA 2533

Qy 1198 TTGGGTCTGACCCCAAGATAAGATCAAGACCCAGCGTGCAGCACTGCGTCCGCGATCAC 1257
Db 2534 TTGGGCTGCGGACGAGGACATCGCACCGCATGCGCGCGCATACAGTCCCGGATCAC 2593

Qy 1258 ACCGAAGATCCAAACACGCTTCCGCGCGAGATACCGGAACTATCACCGCGTACCGCTCA 1317
Db 2594 ACCGAGATCCGGCAACGCTTCCGCGC-GACACGCGCGGATCAGCGGTGCGACCC 2652

Qy 1318 CCAGCGGAGCTGGCGTTCTGTGACGGTGCAGTGCAGTCCGTGGCGGAAATCACCGCA 1377
Db 2653 GCGCGGTGCGGTGTCGCTGAGCGGACGCGCAC-CAACCTGCGCAGAAATCAGCCCG 2711

Qy 1378 CACTTGTACTCCATGCTGTGTAATGACCTGCCGTGTTCCGACTTTCGAACTGCTGT 1437
Db 2712 TACTTCGACTCCATGCTGTGTAAGTGAAGTGTGCG-GGCGGTGACCTCCCTACCGCAGTG 2770

Qy 1438 GCTGTGCACAGCGCGGTGGTGTGAGTTACCGGTGTCTGGTGTGCAACCAACATTTGT 1497
Db 2771 AGCGGTGCGCGCGCGGATCGCGAGTTCGGATCCGCGGGGTATCGACGAATATTCG 2830

Qy 1498 TTCTTGGGTGCGTGTGTCGCGGAGAGGAGACTTCACTTCAAGCGCATCGCCACCGGATTC 1557
Db 2831 TTCCTGCAAGCGGTCTTGGATGACCCGCGACTTCGAGCGGGCGGGTCAACCGTCTTC 2890

Qy 1558 ATTGCGGATCACCGCACCTCTTCAGGCTCCACCTGTGATGATGAGCAGGAGCGCATC 1617
Db 2891 ATTGATGAGCGCGCGCAGCTGTGACCGCGCGGCTCGGCGGACCGCGGACCAAGATC 2950

Qy 1618 CTGGATTACTTGGCAGATGTCAACCGTGAACAAGCTCATGTTGTGCTCCAAAGGATGT 1677
Db 2951 CTTAACTTCTGCGCGCATGTCAACCGTCAACAACCCGTATGGCTCGCTCCGTCAACGATC 3010

Qy 1678 GCAGTCTCTATCGATAAGTGTGCTTAAACATCAAGGATCTGCCACTGCCACGCGTTCCCGT 1737
Db 3011 TACCCGAGCAGCAAGCTGCCGATCTTGATCTCGGGCGCGCACCGCGCGGTCCAG 3070

Qy 1738 GACCGCTGAAGCAGCTTGGCCCGCAGCGCGGTTTGTCTCGTGTCTCGTGAGCAGGACGCA 1797
Db 3071 CAGCGACTAGTCAAGTTGGGGCGGGAAGGATTTGCTCGTTGGTGGGAGTTCGGCGCG 3130

Query Match		14.1%;	Score 509.2;	DB 4;	Length 3492;
Best Local Similarity		49.1%;	Pred. No. 1.1e-134;		
Matches 1661;		Conservative 0;	Mismatches 1668;	Indels 51;	Gaps 10;
Qy	233	TCAAAAAGATCTTGGTAGCAACCGCGGCGAAATCGCGGTCCGTGCTTCCGTGCAGCAC	292		
Db	65	TGAAAAAGGTATTAGTTGCCAATCGTGGCGAAATTGCGAATCGAATTTTGTAGAGCTTGTA	124		
Qy	293	TCGAAACCGGTGCAGCCACCGTAGCTATTATCCCGGTGAAGATCGGGGATCATTCACAC	352		
Db	125	CAGAATTAGATATCCGTACAGTAGCGATTATGCTGCAGAAAGATGATATTCTGTTCATC	184		
Qy	353	GCTCTTTTGTCTCTGAAGCTGTCCGCAATTGGTACCGAAGGCTCACCGATCAAGCGGTACC	412		
Db	185	GTTTCAAGCAGATGAAGCGGTATTAGTTGGTAAGGGGAAAAAACCAATTGAAGCCTATT	244		
Qy	413	TGGACATCGATGAATTTATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTACCCGG	472		
Db	245	TAGACATTGAAAAATATTATCCAAATTGCCAAAAAATCGGAGCAGATGCCATTTCATCCTG	304		
Qy	473	GATACGGCTTCTGTCTGAAATGCCCCAGCTTGCCCGCGAGTGTGCGGAAACGGCATTA	532		
Db	305	GTTATGGCTTTTATCAGAGAACTTACGCTTCGCCGAAGCTTGTGAAGAGAAAGGAATCA	364		
Qy	533	CTTTTATTTGGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAA	592		
Db	365	TTTTTTGTGCGACCTAAACACATCATTTAGATAATTTTGGCGATAAAATTAAGCGAAAG	424		
Qy	593	CCGCCGGAAGAGGCTGGTCTGCCAGTTTGTGGCGGAATC---CACCCCGAGCAAAAAACA	649		
Db	425	AAGCAGCTGTAGCTGCGGGGATTGCTTCGATTCCAGGCTCAGACGGGCCAGTAGCAACGG	484		
Qy	650	TCGATGAGATCGTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGSCAGTTG	709		
Db	485	TGGAAGAGGTTGTAGCTTTTGTGTGAACACATATGGCTTTCCTATCATGATTAAGCTGCTT	544		
Qy	710	CCGGTGTGGCGGACGCGGTATGCGTTTGTGCTTCACTGATGAGCTTCGCAAAATTAG	769		
Db	545	TAGTGTGGCGGCTGCGGGATGCGGTTGCCACGATGTCACAAAGAACACGAGAAAGGTT	604		
Qy	770	CAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGGTATATGTGCAAC	829		
Db	605	ACGAAAGAGCAAAAAGTGAAGCGAAAGCAGCCTTTGGTTCTGACGAGGTTTATGTGTAAG	664		
Qy	830	GTGCTGTGATTAACCTCAGCATATTGAAGTGCAGATCCTTGGCGATGGCGGTATATGTGCAAC	889		
Db	665	AGTATATTCTAATCCTAAACATATCGAAGTACAAATTTTAGGCGATCATCATGGAACG	724		
Qy	890	TTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCTGCACCAAAAAGTTGTGCAAA	949		
Db	725	TCATTGCATTTATTGAACGTGATTGTTCCGTTCAACGCGCGCACCAAAAAGTGTAGAAG	784		
Qy	950	TTGCGCCAGCACAGCATTTTGGATCCAGAACTGCGTGTATCGCATTTGTGCGGATGAGTAA	1009		
Db	785	TCGCACCATGTGTATCAATGAATGAAGAACAAACGAGCAGCCATTGTTCCGCTGCTGTGC	844		
Qy	1010	AGTTCTGCCCTCCATTGGTTACCAGGGCGGGAACCGTGGAAATTTCTTGGTTCGATGAAA	1069		
Db	845	AGTTAATGGCACATGTCCGCTACGTGAATGCGGGAACGGTTGAGTTTTTAGT---AGAAG	901		
Qy	1070	AGGGCAACACAGCTCTTCATCGAAATGAACCCACGTATCCAGTTGAGCACACCGGTGACTG	1129		
Db	902	GGGATCAGTTTATTATTATGAAGTGAATCCTCGTGTTCAGTAGAACATATCATCACAG	961		
Qy	1130	AAGAACTACCGAGGTGGACCTGTGTAAGGGCGCAGATGCGCTGGCTGGTGCACCT	1189		
Db	962	AAATGATTACAGATATTGATATTGTGATCTCTCAATTACAAATTCGCAAGGGCTTGATT	1021		
Qy	1190	TGAAGGAA-----TTGGGTCTGACCAAGATAAGATCAAGACCCACGGTGCAGCACTGC	1243		
Db	1022	TGCATAAAGATATGCAATTTGCCAAAACAAACGAATTGACATTAAGGCGCGGTATTC	1081		
Qy	1244	AGTCCCGCATCACCCAGGAAGATCCAAACACGGCTTCCGCCCAGATACCGGAACATATCA	1303		

Db	1082	AATGTCGATTACGACTGAAGATCCCCTGAACCAAGTTTATGCCAGACACAGGAAATCG	1141		
Qy	1304	CCGGTACCGCTCACCAAGCGGAGCTGGCGTTCGTCT---TGACGGTGCAGTCAAGCTCG	1360		
Db	1142	ATACGTATCGTTTACCAGGTGTTTGGTGTGCGTTAGATGTAGGGAATGCTTATCTG	1201		
Qy	1361	GTGGCGAAATCACCGCACACTTTGACTCCATGCTGCTGTAATAATGACCTGCCGTGGTCCG	1420		
Db	1202	GCTACGCTGTGACTCCCTACTTTGATTCTTTATGGTTAAAGTCTGTACGATGGTTCT	1261		
Qy	1421	ACTTTGAAACTGCTGTTGCTGTGCACAGCGCGGCTGGTGGTGGTTCACCGTGTGGTG	1480		
Db	1262	CTTTTGAACAGGCAATCAGTAAAAATGCAACCGCTGCTTAAAAAGAAATTCGGATTGCTGGCG	1321		
Qy	1481	TTGCAACCAACATTTGTTTCTTGTGCGTGCACAGCGCGGCTGGTGGGAAAGAGGACTTCACTTCCAAAC	1540		
Db	1322	TGAAAACAAAATATTCGGTTTTCACAAAATGTTGTGAGCTATCCAGCGTTTCAATCTGGCG	1381		
Qy	1541	GCATCGCCACCGGATTCATTGCCGATCACCCGACCTCTTCAGGCTCCACCTGCTGATG	1600		
Db	1382	AAGCCAAAACAACCTTTATTGATAATACACCTGAATATTGAATTTCTCTGCTATGCGCG	1441		
Qy	1601	ATGAGCAGGACGCATCCTCGATTACTTGGCAGATGTCCACCGTGAACAAGCCTCATGTTG	1660		
Db	1442	ATCGTGGCAATAAAACGATGAAATACATTGGAGAGTAAACGGTCAATGGGTTCCCTGGCA	1501		
Qy	1661	TGCGTCCAAAGGATGTTGAGCTCCTATCGATAA-----GCTGCCATAACATCAAGGATC	1714		
Db	1502	TTGAAAGAACGGAGAAAAATATTTTGAAGCCCCGCGGTGCCGACAGATATTGAAGTTC	1561		
Qy	1715	TGCCACTGCCACGCGGTTCCCGTGACCGCTTGAAGCAGCTTGGCCAGCCGCTTGTGCTC	1774		
Db	1562	CAGAAAAAGTGATTACAGCTAAAAATATTCTAGACGCTCAAGGAGCAACCGCCGTCATCG	1621		
Qy	1775	GTGATCTCGTGAGCAGGACGCACTGGCAGTTACTGATACCACTTCCGCGATGCACACC	1834		
Db	1622	ATTGGGTTAAGAAATCAAGAAAGTGTGTTAATGACAGATACCACTGTTCCGTGATCGCACCC	1681		
Qy	1835	AGTCTTTGCTTGGACCCGAGTCCGCTCATTCGCACTGAAGCCTTGGCGCAGAGGCCGCTCG	1894		
Db	1682	AAAGTTATTAGCTACTCGTGTGAGAACACAAGATTTTAAAGCAATTGCTGGTCTAACTG	1741		
Qy	1895	CAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCCTGGGCGGCGCGACCTACGATGCG	1954		
Db	1742	ATGCAGCCCTGCCTGAGCTGTTTCTAGTGAATGTGGGTGGCGCTACGTTGATGTTG	1801		
Qy	1955	CGATGCGTTTCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAGGCGGATGC	2014		
Db	1802	CCTATCGTTCTTAAACGAAAGACCCATGGCAACGTTTAAAGAAAAATTCGTCAGTTGATGC	1861		
Qy	2015	CGAATGTAAACATTCAGATGCTGCTTCGCGCGCGCAACACCGTGGGATACACCCCGTACC	2074		
Db	1862	CAAAACACACTTTTACAAATGCTGTTTCAAGAGGATCTAATGCGGTAGGCTATCAAAATATC	1921		
Qy	2075	CAGACTCCGCTGTCGCGGCTTGTAAAGGAAGCTGCCAGTCCGCGGTGGACATCTTCC	2134		
Db	1922	CTGATAATGTTATTGAAGAAATTTATTAAAGAAATCCGCTCGCCAAAGGAGTCGATGTTTTCC	1981		
Qy	2135	GCATCTTCGACGCGTTAAACGACGCTCTCCAGATGCGTCCAGCAATCGACGCGCTCTGG	2194		
Db	1982	GAATTTTGTATAGCTTAAACTGGATTCTCAATGGAAAAAAGTATTCAAGTCGTTCCGG	2041		
Qy	2195	AGACCAACACCGGCTAGCCGAGGTGGCTATGGCTTATTCTGGTGTCTCTCTGATCCAA	2254		
Db	2042	ATACCGGAA---AAATTGCGGAAGCAGCAATTTGTTTACTACTGGGACATCAATGATCCAG	2098		
Qy	2255	ATGAAAAGCTCTACACCTGGATTACTACTAAAGATGGCAGAGGAGATCGTCAAGTCTG	2314		
Db	2099	CCCGAGCAAAATATAATGTTCAATATACCTTTGATATGGTAAAGAAATTGAAAAATTTAG	2158		
Qy	2315	GCGCTCACATCTTGGCCATTAAAGGATATGGTGGTCTGTTTCGCCCAGCTGCGGTAACCA	2374		

Db 2159 GTGCACAAATCAATTCGGATTAAAGATATGGCTGGCTTATTGAAACCAACCAAGCTGCTTATC 2218
QY 2375 AGCTGGTACCGCACTGCGCGCTGAATTCGATCTGCCAGTGCACGTGCACACCCACGACA 2434
Db 2219 GTTTAATTAGTGAATTAAGAGCAGCCACGGAATTTACCAATTCATCTCCACACTCACGACA 2278
QY 2435 CTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCGAGCTCAAGCTGGTGAGATGCTGTTG 2494
Db 2279 CTAGTGGCAATGGGATCATCATATTTAGCAGCTACTAAAGCGGCGTTGATATGTTG 2338
QY 2495 ACGGTGCTTCCGCACCACTGTCTGGCACCACTCCAGCCATCCCTGTCTGCCATTGTTG 2554
Db 2339 ACFTCGCAATGAGTGGATGAGTGGCGCACTAGCCAGCCAAAGTATGAACAGTCTATATT 2398
QY 2555 CTGCAATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTCTGACCTCG 2614
Db 2399 ATGCTTTAGTCAATGGTGAACGGACGCCCACTATTAAACATTGATAATGCACAGAAAATCA 2458
QY 2615 AGCGTACTGGGAAGCAGTGGCGGACTGTACTCTGCCATTTGAGTCTGGAACCCAGGCC 2674
Db 2459 ATCAATTATGGGAAGATGTGGCATGTATTATCAACCAATTTGAAAATGGTTAAATGCC 2518
QY 2675 CAACCGTCCGCTCTACCGCCACGAAATCCAGGCGGACAGTTGTCCAACTGCGTGCAC 2734
Db 2519 CGCAAAACAGAGTCTATATGTCATGAATGCCTGGTGGCAATACTCTAATCTACAGCAGC 2578
QY 2735 AGGCCACCGCACTGGGCTTTGGGATCGTTTCGAACTCATCGAAGACAACACTACGCAGCCG 2794
Db 2579 AAGCAAAAGCGGTAGGCTTAGGGCACCGTTGGGATGAATCAAAAATATATATACACACAG 2638
QY 2795 TTATAGATGCTGGGACGCCCAACCAAGGTCAACCCCTCCTCAAGGTTGTTGGCGACC 2854
Db 2639 TGAATTGATGTTTGGCGATATTGTAAAGTGACGCCCTCTTCAAAAGTCGTGGGAGACA 2698
QY 2855 TCGCACTCCACCTCGTTGGTGGGCTGTGGATCCAGCAGACTTTGCTGCCGATCCACAAA 2914
Db 2699 TGGCACTCTTCATGTTTCAAAATAATCTGACAGAACAGATGTTTATGCGCGTGGTGAAG 2758
QY 2915 AGTACGACATCCAGACTCTGTCTATCGGCTTCTTCCGCGCGAGCTTGGTAACCTCCAG 2974
Db 2759 AACTAAGTTTCTCTGAATCAGTTGTGACTTTTTTCCAGGTGATTTAGGTCAACCACTG 2818
QY 2975 GTGGCTGGCCAGAGCCACTGCGCACCCCGGCACTGGAAGCGCGCTCCGAAGGCAAGGCAC 3034
Db 2819 GTGGGTTCCGAAAGAGCTGCAACGAATTATTCTAAAGGTGACCCAGCTTCAAGAGC 2878
QY 3035 CTCTGACGGA--AGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTTCCAAGG 3091
Db 2879 GGCCAGGTGACTTAGCAGCACCTGTGATTTTTCGAAAGTACAGAAGAAATTAGCCGAAA 2938
QY 3092 AACGTGCAATAGCCTCAACCGCC-----TGCTGTTCCCGAAGCCAA 3133
Db 2939 AAATTGGGTATCAACCTAAATTGGAAGAAGTTTAAAGTTAATTATGTATCCACAAGTAT 2998
QY 3134 CCGAAGAGTTCCTCGAGCACCGTCCGCGCTTCGGCAACACCTCTGCGCTGGATGATCGTG 3193
Db 2999 TTTTAGAGTATCGTCAAAAATACGAACCTTTGGAGATATAACCTTATTAGATACGCCAA 3058
QY 3194 AATTCTTCTACGGCCTGGTCGAAGGCGCGGAGACTTTGATCCGCTGCCAGATGTGGCA 3253
Db 3059 CATTCTTTAATGTTATTCGTCAAGGA---GAGACATTGGAAAGTTCAAATTGAACGAGGAA 3115
QY 3254 CCCCACTGCTGTTGCTGCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGGGCAATG 3313
Db 3116 AAACGTTAATTATTCGTTTAGATGAATGGCGAACCTGATATTGACGGAACCGTGCT 3175
QY 3314 TTGTGGCCCAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGT 3373
Db 3176 TGTCTTCAATTGAATGGGCAACGTCGTGAGGTTTGTAGTTAAAGATGCCTCTATTAAAGT 3235
QY 3374 CTGTCAACCGCAACCGCAGAAAAGGAGATTCCTCCAAAGGCGCATGTTGCTGCAACCAT 3433
Db 3236 CTGCTGTTCAAGTAAACAAAAGGCGGAACCAACTAATAAGAACAAATCGGCGCAACGA 3295

QY 3434 TCGCTGG---TGTGTACCCGTGACTGTTGCTGAAGGTGATGAGTCAAGGCTGGAGATG 3490
Db 3296 TGTCTGTTCTGTTCTACAAGTATTGTTGTTCAAAACGTTGGCGATATAAAGTAGAAAAAGTCA 3355
QY 3491 CAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCA 3550
Db 3356 CGTTGCTGATTACAGAAGCCATGAAAATGGAACGACTATCGAAGCAGCTTTTTCGGGGCA 3415
QY 3551 AAATCGATCGCGTTGTGTT 3570
Db 3416 CGGTAGATCACATTTATGTT 3435

RESULT 7
US-09-134-001C-591
; Sequence 591, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynx Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 591
; LENGTH: 3465
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-591

Query Match 13.4%; Score 486.2; DB 4; Length 3465;
Best Local Similarity 48.4%; Pred. No. 3.9e-128;
Matches 1661; Conservative 0; Mismatches 1718; Indels 54; Gaps 9;

QY 231 ATTCAAAAAGATCTTGGTAGCAAAACCGCGGCAATCGCGGTCCGTGCTTTCCGTGCAGC 290
Db 24 AATAAAGAAATTAATCTGTTGTAACCGTGGTGAATCGCCATTAGAAATTTTAGAGCGGC 83
QY 291 ACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCCGTGAAGATCGGGATCAATCCCA 350
Db 84 AGCAGAATTAATATCAGTACAGTAGCAATTTATTCTAATGAAGATAAAAGTTCGTACA 143
QY 351 CCGCTCTTTTGTCTTCTGAAGTGTCTCGCATTTGGTACGGAAGGCTCACCAGTCAAGCGTA 410
Db 144 TAGATATAAAGCAGATGAATCCTATCTAGTTGGAAGTATTTAGGACCTGCTGAAAGTTA 203
QY 411 CCTGGACATCGATGAATTTATCGTGCAGCTATAAAGTTAAAGCAGATGCCATTTACCC 470
Db 204 TTTGAATATCGAACGTATCATCGAAGTAGCTCTTCGCGCAGGTGTCGATGCAATTCATCC 263
QY 471 GGGATACGCTTCTGTCTGAAATGCCAGCTTCCCGCGAGTGTCCGGAACACGGCAT 530
Db 264 TGGGTATGCTTTTAAAGTGAATGAACAATTTGACGCGCATGTGCTGAGGAAGGCAT 323
QY 531 TACTTTTATGGCCCCAACCCACAGGTTCTTGTATCTCACCGGTGATAAGTCTCGCGCGGT 590
Db 324 TAAATTTATAGTCCGCATCTTTGAACATCTAGACATGTTTGAGATAAGGTTAAGGCTAG 383
QY 591 AACCGCCGGAAGAGGCTGCTGCCAGTTTGGCGG---AATCCACCCCGAGCAAAA 647
Db 384 AACAACTGCTATTAAACGCTAACTTACCTGTAAATCCCGGTACAGATGGTCTTATGAAAG 443
QY 648 CATCGATGAGATCGTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTTGTGAAGGCAGT 707
Db 444 TTTTGAAGCTGCAGAACAGTTTGTCTAATGAAGCAGGTTACCCCACTTATGATTAAGGCCAC 503
QY 708 TGCCGGTGGTGGCGGACCGGATGCGTTTGTGCTTCACTGATGAGCTTCGCAAAATT 767

Db 504 AAGCGTGGCGGTGGTAAAGGTATCGGAATCGTTCGTGAATCAAGCGAATTAGAAGACGC 563
QY 768 AGCAACAGAAAGCATCTCGTGAAGCTGAAGCGGCTTTGGCGGATGGCGGGTATATGTGGA 827
Db 564 TTTCCATCGTGCAGAAATCAGAAGCCGAAAGTCAATTTGGTAAATAGCGAAGTTATATCGA 623
QY 828 ACGTGTGTGATTAACCCCTCAGCATATTTGAAGTGCAGATCCTTTGGCGATCACACTGGAGA 887
Db 624 AAGATATATGTATATCCAAAGCATATAGAGGTTCAAGTTATTTGGTGAATTCGGGAA 683
QY 888 AGTTGTACACCTTTATGAACGTGACTGCTCACTGACGGTCTGTCAGGATCGCATTTGTGCGGATGCAGT 1007
Db 684 TATCAATTCATTTGTATGAAGAGATTTGCTCCGTACAAAGACGTCATCAAAAAGTTGTTGA 743
QY 948 AATTGGCCAGCACAGCAATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGT 1007
Db 744 AGTTGCACCTTCAGTAGGTCTTTCTAAACAAATTAAGAGAGCGAATTTGTGATGCCGCAAT 803
QY 1008 AAAGTTCTGCGCTCCATTTGGTTTACCAGGCGCGGGAACCGTGGAAATTTCTTGGTCCGATGA 1067
Db 804 TCAACTGATGGAATAATAAATACGTCAACGCTGGAACAGTAGAATTTTAGTTCTG- 862
QY 1068 AAAGGCAACACCGTCTTCATCGAAATGAACCCACGTATCCAGTTTGAGCACACCGTGCAC 1127
Db 863 --GGGATGAATTTTCTTCATTTAGGTTAATCCACGTTTCAAGTTGAGCATACAATTAC 920
QY 1128 TGAAGAAAGTCACCGAGGTGGACTGGTGAAGGCGCAGATCGGCTTGGCTGCTGGTCAAC 1187
Db 921 TGAATGATTTACTGGTATAGACATTTGTGAACACGCAAAATTTAGTTGCTAATGGAGAATC 980
QY 1188 CTTGAAGGAATTTGGTCTGACC-----CAAGATAAGATCAAGACCCACGGTGCAGC 1238
Db 981 GTTATTTGGAGATAAAATCTCTATGCCACAGCAAAATGAATTCAAACATTAGGGTATGC 1040
QY 1239 ACTGCAGTCCGTCATCACCCAGGAAGATCCAAACAAACCGGCTTCGCGCCAGATACCGGAAC 1298
Db 1041 GATACAATGTCGTATAACAACCTGAAGATCCTACTAATGATTTTATGCCAGATTTCTGGCAC 1100
QY 1299 TATCACCGCGTACCGCTCACCGAGGAGCTGGCGGTTCTTGAACGGTGCAGCTCAGCT 1358
Db 1101 AATTATTGCATATCGATCAAGTGGCGGTTTGGTGTGAGACTTGTATGCAGGGGATGGATT 1160
QY 1359 C---GGTGGCGAAATCACCGGCACACTTTGACTCCATGCTGGTGAATAATGACCTGCCGTGG 1415
Db 1161 CCAAGGTGCAGAAATTTACCTTACTACGATTCACATATAGTTAAGCTTTCTACACATGC 1220
QY 1416 TTCCGACTTTGAAACTGCTGTGCTGTCGACAGCGCGGTTGGCTGAGTTACCGGTGTC 1475
Db 1221 CGTTTCATTTAAACAGCTGAAGAGAAATGGAAACGTTCAATTACGCGAAATGCGAATTGG 1280
QY 1476 TGTGTTGCAACCAACCATTTGGTTTCTTGGCTGGTGGTGGCGGAAGAGGACTTCACCTTC 1535
Db 1281 TGGCGTAAAGACGAATATTTCCATTTCTCATCAATGTTATGCGTAATGATAAATTTAGAAG 1340
QY 1536 CAAGCGCATCGCCACCGGATTCATTTGCCGATCACCGCACCTCCTTCAGGCTCCACCTGC 1595
Db 1341 TGGTGATTATACTACTAAATTTATTGAAGAAACACCTGAACTTTTCGATATTGCACCCGAC 1400
QY 1596 TGATGATGAGCAGGACGCAATCCTGGATTACTTTGGCAGATGTCAACCGTGAACAAGCCTCA 1655
Db 1401 ATTGGACAGAGGTACCAAGACTTTAGAGTATATTGGTAAATGTGACGATAAACCAGATTTC 1460
QY 1656 TGGTGT-----GCGTCCAAAGGATTTGACGCTCCTATCGATAAGCTGCCTAACATC-- 1707
Db 1461 TAATGTAGAAAAGCGTCCAAAACAGAAATATGAATCTACCAAAATCCCAAAATTTCTCA 1520
QY 1708 -AAGGATCTGCCACTGCCACCGGTTCCCGTGACCGCGCTGAAGCAGCTTTGGCCAGCCGC 1766
Db 1521 AAAGAAAATCAATCAGTTATTTTGGAAACAAAACAAATTTCTTGAGCAACATGGACCAACAGG 1580
QY 1767 GTTTGCTGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACTTCCGCGA 1826

Db 1581 TGTACAAATTTGGTTAGAGAAACAAGAAGATGTTTTAATTACCGATACTACATTTAGAGA 1640
QY 1827 TGCAACACAGTCTTTTGTGCTTGGACCCGAGTCCGCTCATTCGCACCTGAAGCCTCGCGAGA 1886
Db 1641 TGCAACACCAATCTTTTACTTGCACACACGTGTAGAACAAAGATATGATGAACATTGCATC 1700
QY 1887 GGCGTGCAGAAAGCTGACTCTCTGAGCTTTTGTCCGTGGAGGCCCTGGGGCGCGCGACCTA 1946
Db 1701 TAAAACTGCTGAAGTTTTTAAAGATAGTTTTTTCATTAGAAATGTGGGTGGTGCACATT 1760
QY 1947 CGATGTGGCGGATGCGTTTCTCTTTTGAAGATCCGTGGGACAGGCTCGACGAGCTGCGCGA 2006
Db 1761 TGATGTGCGCTATAATTTCTTGAAGAGAATCCATGGGAACGTTTAGAAAAGATTGCGCAA 1820
QY 2007 GGCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCGCGCAACACCCGTGGGATACAC 2066
Db 1821 AGCCATTCGGAATGTGTTATTCCAAATGTTATTACGAGCTTCGAACGCGAGTAGGTTATAA 1880
QY 2067 CCGGTACCCAGACTCCGTTCTGCCGCGGTTTTGTAAAGAAAGCTGCCAGCTCCGCGTGA 2126
Db 1881 AAACATCTCTGATAATGTAAATTAAGAAATTCGTTTCATGAAGTGCAAAAGCTGGTGTAGA 1940
QY 2127 CATTTCCGCTCTTTCGACCGGCTTAACGACGCTCTCCAGATGCGTCCAGCAATCGACGC 2186
Db 1941 TGTTTCCGTATATTCCGACTCATTTGAACTGGGTTGATCAAAATGAAGTAGCGAATGAAGC 2000
QY 2187 AGTCTGGAGACCAACACCGCGGTAGCCGAGGTGGGTATGGCTTATTTCTGTGATCTCTC 2246
Db 2001 TGTTCAAGAAAGCTGGAATGGTATCTGAGGGTACAAATTTGCTATACAGGTGATATTTAAA 2060
QY 2247 TGATCCAAATGAAGACTCTACACCTTGATTAAGGATATGCGTGGTCTGCTTCGCCAGCTGC 2306
Db 2061 TGCTGAACGTTCCATATATTATATACCTTTAGATTTATACGTTAAATGGCTAAAGAACTGA 2120
QY 2307 CAAGTCTGGCGCTCACATCTTGGCCATTAAGGATATGCGTGGTCTGCTTCGCCAGCTGC 2366
Db 2121 AAGAGAAGGATTCATATATATTAGCAATTAAGATATAGGCTGGTTTATTGAAACCCGAAAGC 2180
QY 2367 GGTAACCAAGCTGGTCAACCGCACTGCGCGTGAATTCGATCTGCCAGTGACGTCACAC 2426
Db 2181 AGCTTACGAATTAATTGGTGAATTACGTGAGGCAACACATCTTCCAATTCATTTACATAC 2240
QY 2427 CCACGACACTGCGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCTGGTGAGA 2486
Db 2241 ACATGATACTAGTGGAATGGATTTGTGACATATAAACAAGCAATTTGATGCTGGCGTGA 2300
QY 2487 TGCTGTTGACGGTGTTCGCGACCACTGTCTGGCACCACTCCAGCCATCCCTGTCTGC 2546
Db 2301 TATTATAGATACTGCTGTTGCATCTATGAGTGGTTTAAACGAGTCAACCAAGTGCAAATTC 2360
QY 2547 CATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTC 2606
Db 2361 ATTATATTATGCACATAAATGGATTTCCACGTAATTAAGAACTGATATTGATGGGTAGA 2420
QY 2607 TGACCTCGAGCCGTACTGGAAGCAGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAAC 2666
Db 2421 AGAGTTGAGTCATTACTGTTCTGTAGTCAGACCTTACTATGCAGACTTTGAGAGTGATAT 2480
QY 2667 CCCAGGCCCAACCGGTGCGGCTTACCGCCACGAAATCCAGGGGACAGTTGTCCAACTT 2726
Db 2481 CAATCACCAAATACAGAAATTTATCAACATGAATGCCAGGTGGCCAATATTCAAACCTT 2540
QY 2727 GCGTGCACAGGCCACCGCACTGGGCGCTTGGGATCGGTTTCGAACTCATCGAAGACAACCTA 2786
Db 2541 AAGTCAACAAGCTAAAAGTTTAGGATTGGGCGAACGTTTTGATGAAGTCAAAAGAGATGTA 2600
QY 2787 CGCAGCGGTTAATGAGATGTTGGGACGCCCAACCAAGGTCAACCCCATCTCTCCAGGTTGT 2846
Db 2601 TCGTGTGTCAACTTCTCTGTTGGAGATCTTTGTAAGATTAACCACTCTTCAAAGTAGT 2660
QY 2847 TGGCGACCTCGCACTCCACCTGTTGGTGGGTGGGTGGATCCAGCAGACTTTTGTGCTGCCGA 2906
Db 2661 TGGAGATATGGCACTATATATATGGTGCAAAATGATCTTGATGAAGATACGGTCAATGA 2720

QY 2907 TCACAAAAGTACGACATCCAGACTCTGTGTCATCGGTTCTCGCGCGGAGCTTGGTAA 2966
Db 2721 TGGTTATAAATAGATTTCACGAAATCTGTTGTGTCATCTTTAAAGGTGACATGGACA 2780
QY 2967 CCCTCCAGGTGGTGGCCAGAGCCACTGCGGACCCGCGCACTGGAAGCCGCTCCGAAGG 3026
Db 2781 ACCTGTCAACGGATTCACAAAGAAATTCGAAGATGTTATTTTAAAGGACAGCAACCAAT 2840
QY 3027 CAAGGCACCTGTACGGAAGTTCCTGAGGAAGAGCAGGGCGACCTCGACGCTGATGATTC 3086
Db 2841 TACTGAAAGACCAGGTGAATACTTGGAGCCGCTCGATTTTGAAGCAATCCGTCAAGAAAT 2900
QY 3087 CAAGGA-----ACGTGCAATAGCCTCAACCGCCTGCTGTTCCT 3125
Db 2901 AAGCGACATACAAAGACGAGGTAAACAGAAAGATATAATTAAGTATGACTTTATCC 2960
QY 3126 GAAGCCAAACCGAAGATTCTCTGAGCACCGTCCGCTTCCGGCAACACCTCTGCGTGA 3185
Db 2961 GAAGGTATATAAACAATATATTCAACCGAAGAGCAATTTGGTAAATGATCTTTACTGGA 3020
QY 3186 TGATCGTGAATCTTCTACGGCCTGCTGTCGAGGCGCGGAGACTTTGATCCGCTGCCAGA 3245
Db 3021 TACACCGACATCTTATTGGCATGCGTAATG---GTGAAACAGTGAATTAATGA 3077
QY 3246 TGTGCGCACCCACTGCTGTTGCTGCTGAGTGGATCTCTGAGCCAGACGATAGGGTAT 3305
Db 3078 TACTGGTAAACGCTCTAATTAATTAATTAAGAAACAAATCAGTGAACCAAGTGAATGGTAA 3137
QY 3306 GCGCAATGTTGTGGCCAAACGTCACCGCCAGATCCGCGCCCAATGCGTGTGCGTACCGCTC 3365
Db 3138 GCGTACAATTTATTACGCTATGAATGGTCAAGCAAGACGTATCTATATCAAGATGAAAA 3197
QY 3366 CGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGAGATTCCTCCAACAGGCGCCATGTTGC 3425
Db 3198 TGTAAACGGAATGCTAATGTTAAACCTAAGCGGATAAATCAAAATCCAATCATATTTGG 3257
QY 3426 TGACCAATTCGCTGGTGTGTGTACAC---CGTGAATGTTGCTGAAGGTGATGAGGTCAAGGC 3482
Db 3258 TGCTCAAAATGCTGTTCTGTAACTGAAGTCAAAAGTGTCTGTAGGCGATGAAGTTCGAAGC 3317
QY 3483 TGGAGATGAGTGCATCGCAATCAATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCTGT 3542
Db 3318 TAATCAGCCATTATTAACTCACTGAAGCAATGAAGATGGAACGACGATTGAGGCACCAAT 3377
QY 3543 TGACGCAAAATCGATCGCGTGTGTTGTTCTCTGCTGCAACGAAGGTGGAAGTGGCGACTT 3602
Db 3378 TGATGGAATTAATAACAAATCAATGTTGTTCTAATGGAGATGCCATTGCCACAGGAGATTT 3437
QY 3603 GATCGTCGTCGTT 3615
Db 3438 ATTAGTGGAAATT 3450

RESULT 8
US-08-956-171E-324/c
; Sequence 324, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA

ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 324:
SEQUENCE CHARACTERISTICS:
LENGTH: 5030 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 324:
US-08-956-171E-324
Query Match 13.3%; Score 479.8; DB 4; Length 5030;
Best Local Similarity 48.3%; Pred. No. 3.3e-126;
Matches 1657; Conservative 0; Mismatches 1722; Indels 54; Gaps 9;
QY 231 ATTCAAAAAGATCTTGGTAGCAAAACCGCGCGGAAATCGGGTCCGTGCTTCCGTGCAGC 290
Db 3846 AATAAAAAGTTACTTGTGCTAACCGTGGAGAAATTCGAATTCGTATATTCAGAGCGGC 3787
QY 291 ACTGAAACCGGTGCAGCCACGGTAGCTATTATACCCCGTGAAGATCGGGATCATTTCCA 350
Db 3786 GGCAGATTAGACATCAGCACAGTTGCAATTTATTCGAATGAAGACAAAAGTTCATTACA 3727
QY 351 CCGCTCTTTTGTCTGAAGCTGTCCGCAATTCGTTACCGAGGCTCACCAAGGCGTA 410
Db 3726 TAGATATAAGCAGATGAATCCTATTATTAGTTGGAAGTGAATTTAGTCTCTGCTGAAAGTTA 3667
QY 411 CCTGGACATCGATGAATATTCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTTACCC 470
Db 3666 TTAAATATTGAGCGGTATCATTTGATGTAGCAAAACAAGCGAATGTGGATGCGATTCATCC 3607
QY 471 GGGATACGGCTTCTGCTGTAATAATGCCAGCTTTCGCCGAGTGTGCGGAAAACGGCAT 530
Db 3606 TGGCTATGGATTTTAAAGTGAATAATGAACAATTTGCGCGTCTGTTGTGAGAGGAAT 3547
QY 531 TACTTTTATTTGGCCCAACCCCGCAGAGGTTCTTTGATCTCACCGGTGATAAGTCTCGCGCGGT 590
Db 3546 TAAATTTATTTGGTCTCTCATTTAGAACATTTAGATATGTTTGGAGATAAAGTTAAAGCTCG 3487
QY 591 AACCGCGCGAAGAGGCTGCTGCCAGTTTGGCGGAATCCACCCCGAGCAAAAACAT 650
Db 3486 TACAACGGCTATCAAGGCGAGATTACCAAGTTATTCCTGTACAGACGGTCCCAATTAATC 3427
QY 651 CGATGAGATCGTTAAAGCGCTGAAGGCGCCAGAC---TTACCCCATCTTTTGTGAAGGCGAGT 707
Db 3426 ATATGAATTAGCAAAAGAAATTTTCAGAGAAGCTGTTTCCCGCTAATGATTAAGGCCAC 3367
QY 708 TGCCGGTGGTGGCGGACCGCGGTATGCGTTTGTGCTTACCTGTAGCTTCGCAAAAT 767
Db 3366 AAGTGGTGGCGCGGTAAAGGTATGAGAATCGTTCGTGAAGAAAGTGAATTAGAAGTGC 3307
QY 768 AGCAACAGAGCATCTCGTGAAGCTGAAGCGGCTTTTCGGCGATGCGCGGTATATGTGCA 827

Db 3306 TTTCCATAGACAAAATCAGAAGCTGAAAAATCATTTGGTAATAGTGAAGTTTACATAGA 3247
Qy 828 ACGTGTGTGATTAACCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGA 887
Db 3246 AAGATACATTGATAATCCAAAGCAATATGAAGTACAAGTACATAGGTGACGAACATGGA 3187
Qy 888 AGTTGTACACCTTTATGAACGTGACTGCTCACTGACGCTGCTGCACCAAAAAGTTGTGGA 947
Db 3186 TATCGTACACTTATTTGAACGTGATTGTTAGTACAACGCTGCTCATCAAAAAGTTGTAGA 3127
Qy 948 AATTGGCCGACACAGCATTTGGATCCAGAACTGCGTATCGCATTTGTGCGGATGCAAT 1007
Db 3126 AGTTGCACCATCAGTTGGATTATCATCAACATTACGTCAACGTAATTTGTGATGCTGCAAT 3067
Qy 1008 AAAGTTCTGCCGCTCCATTGGTTACCAAGGCGCGGGAACCGTGGAAATCTTGGTGCATGA 1067
Db 3066 TCAATTGATGGAATAATATAATATGTCATGCAAGTACTGTTGAATTTCTAGTATCTG- 3008
Qy 1068 AAAGGGCAACCAAGTCTTCATCGAAATGAACCCACGTAATCCAGGTTGAGCACACCCGTGAC 1127
Db 3007 --GTGACGAATTTCTTTTATAGAAAGTTAAACCTCGTGTACAAGTAGAGCATACAATTAC 2950
Qy 1128 TGAAGAAGTCAACGAGGTGGACCTGGTGAAGCGCGCAGATGCGCTTGGCTGCTGGTGCAC 1187
Db 2949 AGAGATGGTAAACAGGAATTGATATTGTTAAGACACAAATTTTAGTTGCAGCAGGTGCCGA 2890
Qy 1188 CTTGAAGGAATTGG-----GTCTGACCCAAAGATAAGATCAAGACCCACGGTGCAGC 1238
Db 2889 TTTATTTGGTGAAGAGATTAATATGCCGGCAACAAAAGATATTACAACATTAGGCTATGC 2830
Qy 1239 ACTGCAGTCCCGATCACCACGGAAGATCCAAACAAACGGCTTCCGCCAGATACCCGGAAC 1298
Db 2829 CATCCAATGCTGATTAACAACAGAAAGATCCGTTAAATGATTTTCATGCCGGATACCTGGAAC 2770
Qy 1299 TATCACCGGTACCGTCCACGAGCGGAGCTGGCGTTTCGTTGACCGTGCAGCTCAGCT 1358
Db 2769 AATCATTTGCTTATCGTTCAAGCGGGGGCTTTGGTGTACGCTTGTATGCTGGAGATGGTTT 2710
Qy 1359 C---GGTGGCGAAATCACCGCACACTTTGACTCATGCTGGTGAATAATGACCTGCCGTGG 1415
Db 2709 CCAAGGTGCTGAGATATCACCTTATTATGATTCAATTAATCTGTAAATTTATCTACACAGC 2650
Qy 1416 TTCCGACTTTGAAACTGCTGTGCTGTCGACAGCGCGCTTGGCTGAGTTCACCGTGC 1475
Db 2649 GATATCATTTAAACAAGCAGAAGAAAAAATGGTACGCTCATTACGAGAAATGCGTATTTCG 2590
Qy 1476 TGGTGTGCAACCAACATTGGTTTCTTGGTGGCTGCTGCGGGAAGAGACTTCACCTTC 1535
Db 2589 TGGTGTAAAACATAATTCATCTTAAATTAATGAATGAAGAAATAAAAAGTTTCAACAG 2530
Qy 1536 CAAGCGCATGCCACCGGAATTCATGCGGATCACCGCACCTCCTTCAGGCTCCACCTGC 1595
Db 2529 TGGTGATTACACAACATAAATTTATTGAAGAAACACCAAGAACTTTTCGACATTCAGCCGTC 2470
Qy 1596 TGATGATGAGCAGGACGCACTCCTGGATTACTTTGGCAGATGTCAACCGTGAA-----C 1647
Db 2469 TCTAGATAGAGGTACTAAAACATTAGAATATATAGGTAATGTAAACAATTAATGGTTTCCC 2410
Qy 1648 AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTGCTAACAATC 1707
Db 2409 AATGTTGAGAAACGTCCTCGAAACAGACTATGAATTAGCATCAATTCCAACTGTATCTTC 2350
Qy 1708 AAG-GATCTGCCACTGCCACGCGTTCCCGTGACCGCTGAAGCAGCTTGGCCGACGCGC 1766
Db 2349 AAGTAAATCGCTTCATTTAGTGTGACGAAACAATTTGCTTGTATGAAGTAGTCCAAAAGG 2290
Qy 1767 GTTTGCTGCTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACTTCGCGGA 1826
Db 2289 TGTAGCTGAATGGGTTAAAAGCAGGATGATGTCTTACTTAACAGATACAACCTTTAGAGA 2230
Qy 1827 TGCACACCAAGTCTTTGCTTGGACCCGAGTCCGCTCATTCGCACCTGAAGCTTGGGCGAGA 1886
Db 2229 TGCACACCAATCATTTATAGCTACAGGATTAGAACTAAGGATATGATTAATATCGCATC 2170

Qy 1887 GGCCGTCGCAAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCTGGGCGGCGACCTA 1946
Db 2169 CAAAACAGCGGACGTATTTTAAAGATGGTTTCTCACTAGAAATGTGGGCGGTGCTACATT 2110
Qy 1947 CGATGTGCGGATCGGTTTCTCTTTGAGGATCCGTGGGACAGGTCGACGAGCTGCGCGA 2006
Db 2109 TGATGTGGCATATAATTTCTTGAAGGAAAAACCATGGGAAACGACTTGAACGCTACGTAA 2050
Qy 2007 GGCGATGCCGAATGTAAACATTCAAGATGCTGCTTCCGCGCCGCAACACCGTGGGATACAC 2066
Db 2049 AGCTATTCCAATGTATTATTCCAATTTGTTACGTCCTTCAACGCAAGTTGGTTATAA 1990
Qy 2067 CCGGTACCCAGACTCCGTCCTGCCGCGGTTTGTAAAGGAAGTGCAGCTCCGCGGTGGA 2126
Db 1989 AAACATATCCTGATAATGTTATTTCATAAATTCGTACAAGAAAGTGTAAAGCAGGCATAGA 1930
Qy 2127 CATCTTCCGCACTTTCACGCGCTTAAACGACGCTCTCCAGATGCGTCCAGCAATCGACGC 2186
Db 1929 TGTCTTTAGAAATTTTCGATTCATTAACCTGGGTAGATCAAAATGAAGTTGCCAATGAAGC 1870
Qy 2187 AGTCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTTGGTATCTCTC 2246
Db 1869 AGTACAAGAAAGCGGCAAAATCTCAGAAGGTACTATTTGTTATACAGGTGACATTTTAAA 1810
Qy 2247 TGATCCAAATGAAAAGCTCTACACCTCGATTACTACCTAAAGATGCGAGAGGAGATCGT 2306
Db 1809 TCCTGAGCGATCAAAACATTTATCTTTAGAGTATTATGTCAAACCTAGCTAAAGATTAGA 1750
Qy 2307 CAAGTCTGGCGCTCACATCTTGGCCATTAAAGGATATGGCTGGTCTGCTGCCCGAGCTGC 2366
Db 1749 ACGTGAAGGTTTCCATATTTTAGCGATTAAAGATATGGCAGGCTTATTAACCTAAAGC 1690
Qy 2367 GGTAAACCAAGCTGGTCAACCGCATGCGCGCGTGAATTCGATCTGCCAGTGCACGTCACAC 2426
Db 1689 CGCTTACGAATTGATGGTGAAGTTAAATCAGCTGTAGATTTACCAATTCATCTTCACAC 1630
Qy 2427 CCACGACACTGCGGTTGCCAGCTGGCAACCTACTTTGTCGAGCTCAAGCTGGTGCAGA 2486
Db 1629 TCATGATACAAGTGGTAATGGTTTATTAAACATACAAACAAGCAATAGATGCTGGTGCGA 1570
Qy 2487 TGCTGTTGACGGTGTCCGCAACCACTGTCTGGCACCACTCCAGCCATCCCTGTCTGC 2546
Db 1569 TATCATTGATACTGCTGTGCTTCAATGAGTGGTTTAAACAAGTCAGCCACGCGCAATTC 1510
Qy 2547 CATGTTGTGCTGCTTCCGCGCACACCGCTCGCGATACCGGTTTGAGCCTCGAGCTGTTTC 2606
Db 1509 GTTATATTATGCATTAATGGCTTCCACGCGCACTAGAACTGATATTGAAGGTATGGA 1450
Qy 2607 TGACTCTGAGCCGTACTGGAAGCAGTGGCGGAGTGTACCTGCCATTTGAGTGTGGAAC 2666
Db 1449 GTCACTTAGTCATTTATGCTCAACTGTACGTAATTTATTATTATTATTGAAAGTGATAT 1390
Qy 2667 CCCAGGCCCAACCGGTCGCTCTACCGCCACGAAATCCAGGCGGACAGTTGTCCAACT 2726
Db 1389 CAAATCACCGAATACTGAATAATTTATCAACATGAATGCTGGTGGACAGTATTCGAATTT 1330
Qy 2727 GCGTGCACAGGCCACCGCACTGGGCTTGGCGATCGGATCGGTTTCGAACTCATCGAAGCAACTA 2786
Db 1329 AAGTCAACAAGCTAAAAGTTTAGGTTTAGGCGAAAGATTTGATGAAGTCAAAGATATGTA 1270
Qy 2787 CGCAGCGGTTAATGAGATGCTGGGACGCCCAACCAAGGTCAACCCCATCTCCAGGTTGT 2846
Db 1269 TCGCAGAGTGAATTTCTTATTGCTGATATCGTAAAGTAAACCACTCGTCTAAAGTAGT 1210
Qy 2847 TGGCGACCTCGCACTCCACCTGCTGGTGGGCTGGGTTGGATCCAGCAGACTTTGCTGCGGA 2906
Db 1209 TGGTGATATGGCACTTTATATGCTACAAAATGATCTTGATGAACAAATCCGTGATTACAGA 1150
Qy 2907 TCCACAAAAGTACGACATCCCAAGACTCTGTCTCGCTTCTCGCGGCGGAGCTTTGGTAA 2966
Db 1149 TGGCTATAAATTAGATTTCCCAAGATCAGTAGTGTCTTCTTCAAGGTGAAATAGGACA 1090


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QY 2967 CCCTCCAGGTGGTGGCCAGAGCCACTGCGCACCCGCGCACTGGAAGCGCGCTCCGAAGG 3026
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Db 1089 ACCTGTAATGGTTTAAATAAAGATTACAAGCGGTATTTTAAAGGCCCAAGAGCACT 1030
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3027 CAAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATC 3086
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1029 AACAGCTCGTCCAGGTGAATATCTAGAGCCAGTTGATTTTGAAAAAGTCCGTGAGTTGCT 970
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3087 CAAGGAACGTGCAATAGCC-----TCAACCGCCTGCTGTTCCC 3125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 969 TGAAGAAGAGCAACAAGGTCTGTTCGGAGCAAGATATTTATGTTATGTAATATCC 910
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3126 GAAGCCAAACGGAAGTTCCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGA 3185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 909 AAAAGTATATGAACAATATATTCAAACCTAGAAATCAATACGGAACCTTATCGTTACTTGA 850
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3186 TGATCGTGAATCTTCTACGGCCTGTGTCGAAGCCGCGAGACTTTGATCCGCTGCCAGA 3245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 849 TACGCCTACATCTTCTTTGGAATGCGTAATG--GTGAACAGTAGAAATCGAAATCGA 793
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3246 TGTGCGCACCCCACTGTTGTCGCCCTGGATCGCATCTCTGAGCCAGACGATAAGGGTAT 3305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 792 TAAAGGTAAACGATTAAATTAATAACTAGAAACGATTAGTGAACCCAGATGAAATGGTAA 733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3306 GCGCAATGTTGTGGCCAAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTC 3365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 732 TAGAACGATTTACTATGCGATGAATGGTCAAGCGAGACGTATTTTACATTAAGATGAAAA 673
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3366 CGTTGAGTCTGTACCGCAACCGCAGAAAAAGGCAAGATTCCTCCAACAGGCGCATGTTGC 3425
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 672 TGTGCATACAAATGCGAAGCTTAAGCCAAAGCAGATAGAGTAATCCAAGTCATATCGG 613
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3426 TGCAACATTCGCTGGTGTGTGTACAC---CGTGACTGTTGCTGAAGGTGATGAGGTCAAGGC 3482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 612 TGCTCAAATGCCAGGTTTCAAGTAACTGAAGTCAAGGTAGTGTAGGTGAAACTGTGAAGC 553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3483 TGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCTGT 3542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 552 TAATCAGCCGTTGCTAATTACTGAAGCTATGAAATGGAATGGAACCAACAATTCAGCACCAT 493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3543 TGACGGCAAAATCGATCGCGTTGTGTTTCCCTGCTGCAACGAAGGTGGAAGGTGCGGACTT 3602
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 492 TGACCGTGTGATTAAACAAGTAACTGTAAATAATGTTGACACAATAGCGACAGGCGGATTT 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3603 GATCGTCGTCGTT 3615
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Db 432 ATTAATCGAAATT 420
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RESULT 9
US-09-107-532A-1156
; Sequence 1156, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2922 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...2922
; SEQUENCE DESCRIPTION: SEQ ID NO: 1156:
US-09-107-532A-1156
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Query Match 13.2%; Score 476.2; DB 4; Length 2922;
Best Local Similarity 49.9%; Pred. No. 2.5e-125;
Matches 1425; Conservative 0; Mismatches 1408; Indels 24; Gaps 8;

QY 199 GTGTCGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAACCGC 258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GTTTATAATAAAAAAAGATGTAGGAGTGGTTCGATGAAAAAAGTTTTAGTTGCTAACAGG 60
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QY 259 GCGGAAATCGCGGTCGCTGCTTCCGTGCAAGCACTCGAAACCGGTGACGCCAGGTAGCT 318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GGTGAATCGCTGTACGTGTATTTTCGTGCTTGTACAGAAATTAGGAATTAATAAACTGTTGA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 319 ATTTACCCCGTGAAGATCGGGGATCAATCCACGCTCTTTTGTCTTCTGAAGCTGTCCGC 378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 ATCTATGCAGAAAAAATGAATATTCGGTACACGCTTCAAAGCGGATGAAGCATATTTA 180
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QY 379 ATTGTTACCGAAGGCTCACCAGTCAAGGCGGTACCTGGACATCGATGAAATATCGGTGCA 438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GTAGCAAGGAAAAAACCAGATTTCCGTATACGCTTCAAAGCGGATGAAGCATATTTCTATC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 439 GCTAAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCTGTCTGAAAAATGCC 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GCGAAAGATCGGAGCTGACGCTATTCATCCGGGTACGGTCTTTTGTGCGAAAAACTTG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 499 CAGCTTCCCGCGAGTGTGCGGAAAAACGGCATTTACTTTTATTGGCCCCAACCCAGAGGTT 558
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 AATTTGCGCAACGGTGCAGGAAAAAGGCATCATTTTGTGGACCCCAACTGCATCAT 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 559 CTTGATCTCACCGGTGATAGTCTCGCGGGTAAACCGCGCGGAAGAGGCTGG---TCTG 615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 TTAGATATTTTGGAGATAAATCAAAGCAAAAGCTGCAGCTATCGAAGCGGGGATGCT 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 616 CCAGTTTGGCGGAATCCACCCCGAGCAAAAAACATCGATGAGATCGTTAAAAAGCGCTGAA 675
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 TCGATTCAGGCACAGATGGACCAATCGCTTCTATAGCAGATCGCTTGGAGTTTGGGAAA 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 676 GGCCAGACTTACCCCATCTTTTGAAGGCAGTTGCGCGGTGGTGGCGGACCGGATGCGT 735
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Db 481 CAATACGGTTATCCGATTATGATCAAGGCAGCTCTATGCGCGCGGCGGACCGGCGATGCGT 540
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QY 736 TTTGTTGCTTCACTGTAGCTTCCCAAATTAGCAACAGAGCATCTCGTGAAGCTGAA 795
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GTAGCTCAGGATGAAAAAGAGTGAAGAGGCTACGAACGTGGGAAAAAGCAAGCAAAA 600
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Db 2755 ACTTTCTTCCAAAGGAGAACTAGGGCAACCCGTTGGCGGATTTCCTAAAAAATTGCAAAAG 2814

QY 3001 CGCGCACTGGAAGCCGCTCCGAAGGCAAGGCACCTC 3037

Db 2815 ATTATCTTAAAGGCAGACCTGCATTGAATGAACGTC 2851

RESULT 10

US-09-543-681A-1699

; Sequence 1699, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 1699

; LENGTH: 1362

; TYPE: DNA

; ORGANISM: Proteus mirabilis

US-09-543-681A-1699

Query Match 8.7%; Score 313.4; DB 4; Length 1362;

Best Local Similarity 55.4%; Pred. No. 4.4e-79;

Matches 721; Conservative 0; Mismatches 556; Indels 24; Gaps 5;

QY 236 AAAAGATCTTGGTAGCAAAACCGCGGCGAAATCGCGGTCCGTCGTTCCGTGCAGCACTCG 295

Db 20 AAAAATCCTCATTTGCCAACCGTGGTGAATTCGACTGCGTATCCTAAGAGCTTGTAAAG 79

QY 296 AAACCGGTGCAGCCACCGTAGCTATTATACCCCGTGAAGATCGGGATCATCTCCACCGCT 355

Db 80 AACTTGGGATCAAAGCATCGCCGTTTCACTCCAGCGCAGACCGTGATTTAAACACGTTT 139

QY 356 CTTTGTCTTGAAGCTGTCCGATTTGGTACCGAAGGCTCACCAAGTCAAGGCGTACCTGG 415

Db 140 TGCTGGCAGACGAGACTATCTGTATTGGTCCCGTCTTCAGCA---AAAAGTTACTTAA 196

QY 416 ACATCGATGAAATATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTTACCCGGAT 475

Db 197 ATATTCGGCAATTATTGCCGCGGCAGAGATAAGTGGCGCAAGCCATTCAACCCAGGAT 256

QY 476 ACGGCTTCCTGTCTGAAATGCCAGCTTGCCCGGAGTGTGCGGAAACGGCATTACTT 535

Db 257 ATGGCTTCCTGTCTGAAATGCCGATTTTGGCGGAAACAGTTGAACGCTCAGGCTTTATTT 316

QY 536 TTATGGCCCAACCCAGAGTTCTTGATCTCACGGTGATAAGTCTCGCGCGTAAACCG 595

Db 317 TTATGGCCCTAAAGCGGAAACCATTCGCCCTAATGGGTGATAAAGTTTCGCTATTGAAG 376

QY 596 CCGGGAAGAGGCTGCTGCGCAGTTTGGCGGAATC-----CACCCCGAGCAAAAAACA 649

Db 377 CGATGAAAAAAGCCGCTGTCTGTGTACCCAGGCTCAGATGGCCCATTTAGGTAACGATA 436

QY 650 TCGATGAGATCGTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTG 709

Db 437 CAGCAAAAATATCGAAATCGCCAAACGCAATTGGTTACCTGTTATCATCAAGCATCAG 496

QY 710 CCGGTGGTGGCGGACCGGTATGCGTTTGTGTTGCTTACCTGATGAGCTTCGCAATTAG 769

Db 497 GTGGTGGCGGTGGTCCGCGTATGCGTGTGTTGCTCGCTCAAAAAAGACTTAGCGCAAGCAA 556

QY 770 CAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTGGAAC 829

Db 557 TCTCCATGACCCGTGCGGAAGCCAAAGCGGCATTTAGCAACGATATGGTCTATATGGA 616

QY 830 GTGCTGTGATTAAACCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAG 889

Db 617 AGTACCTTGAAAAATCCACGCCACCTCGAAATTTCAGGTGATGGCCGATGGACAAGGTAATG 676

QY 890 TTGTACACCTTTATGAACGCTGACTGCTCACTGCGAGCGTCTGTCACCAAAAAGTTGCGAAA 949

Db 677 CTATCTATTAGCTGAACGCTGACTGCTCAATGCAACGTCGCCACCAAAAAGTTGTAAG 736

QY 950 TTGGCCGACGACAGCATTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAA 1009

Db 737 AAGCACGACGACCGGGTATTACCCCTGAGATCCGTAAAAATATCGGTGAACGCTGTGCA 796

QY 1010 AGTTCTGCCGCTCCATTGGTTACCGAGGCGCGGAAACCGTGAATTTCTTGGTCGATGAA 1069

Db 797 ATGCTGTATTGAAATTTGGCTACCGCGGTGCGGTACGTTTGAATTC---CTCTATGAAA 853

QY 1070 AGGCAACGACGCTCTTCATCGAAATGAACCCACGATATCCAGGTGAGCACACCGTGACTG 1129

Db 854 ATGGCGAATTTACTTTATCGAAATGAATACCCGTTATTCAGGTGAGCATCTCTGTTACTG 913

QY 1130 AAGAAGTCAACGAGGTGGACCTGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCT 1189

Db 914 AGATGATCACCGGTGTTGACCTTATCAAAAGAGCAACTGCGTATGTCATCAGGCTTACC-- 971

QY 1190 TGAAGGAATTGGTCTGACCCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCC 1249

Db 972 -----ATTATCAGTCACGCAAGATCAAAATTCACGTTATGACATGCTATTGAGTGCC 1024

QY 1250 GCATCACCAACGGAAGATCCAAACACCGGCTTCCGCCACGATACCGGAACCTATCACCGCGT 1309

Db 1025 GTATCAACGCAAGATCCAAAA---CCTTCTTGCCAAAGCCCGGAAACCATCACTCGTT 1081

QY 1310 ACCGCTCACAGCGGAGCTGGCGTTCTGCTTTCAGGTCAGCTCAGCTCGGTGGCGAAA 1369

Db 1082 TCCACTCACAGCGGATTTGGTGACGTTGGGAATCACAATATTACGCAAGTTACACCG 1141

QY 1370 TCACCGCACACTTTGACTCCATGCTGTGAAATGACCTGCCGCTGCTCCGACTTTGAAA 1429

Db 1142 TTCCACCACACTATGATTCATGATTGGTAAATTCATCTTACGTTGAAACACGTTGAAA 1201

QY 1430 CTGCTGTTGCTCGTGCAAGCGCGCTGCTGCTTTCAGGTCAGCTCAGCTCGGTGGCGAAA 1489

Db 1202 TTGCGATTTCTCGTATGAAAAATGCGTTGGCAGAACTTATTATTGACGCGCATTAACCA 1261

QY 1490 ACATTGGTTTCTTGGCTGCTGCTGCGGGAAGAGGACTTC 1530

Db 1262 ATATTGAGCTACACCAATTCAATATGATGATGAGCAATTC 1302

RESULT 11

US-07-956-700B-5

; Sequence 5, Application US/07956700B

; Patent No. 5539092

; GENERAL INFORMATION:

; APPLICANT: Robert Haselkorn and Piotr Gornicki

; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA

; TITLE OF INVENTION: Carboxylase

; NUMBER OF SEQUENCES: 116

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: 321 No. 5539092th Clark Street

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60610

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/956,700B

; FILING DATE: 19921002

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

TELEFAX: 1-312-755-4489

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1362 base pairs

TYPE: Nucleic acid

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Oligonucleotide

US-08-476-537-5

Query Match 8.6%; Score 313; DB 1; Length 1362;

Best Local Similarity 53.9%; Pred. No. 5.7e-79;

Matches 718; Conservative 0; Mismatches 600; Indels 15; Gaps 3;

Qy 232 TTCAAAAGATCTTGGTAGCAACCGCGCGGAAATCGCGTCCGTTTCCGTGCAGCA 291

Db 7 TTCACAAGATCTTGTATCGCAATCGCGCGGAAATCGCCCTGCGCATCTCCGCACATTGT 66

Qy 292 CTCGAAACCGGTGCAGCCACGGTAGCTATTACCCCGTGAAGATCGGGGATCATTTCCAC 351

Db 67 CAAGAACTCGGATCGGCACGATCGCCGTTCACTCTGATGGAATCGCAACGGCTCCAT 126

Qy 352 CGCTCTTTTGTCTGAAAGCTGTCGCAATTTGACCGAAGGCTCACAGTCAAGCGGTAC 411

Db 127 GTCAGTTAGCGGACGAAGCGGTCTGTATTGG---CGAAGCGGCCAGCAGCAAAAGCTAT 183

Qy 412 CTGGACATCGATGAAATATCGGTGCAGCTAAAGTTAAAGCAGATGCCATTACCCG 471

Db 184 CTCAATATCCCAACATCATTTGCGGCGCCCTGACCCCTTAATGCCAGCGCCATTACCCCC 243

Qy 472 GGATACGGCTTCTGTGAAAATGCCAGCTTGGCCGCGAGTGTGCGGAAACGGCATT 531

Db 244 GGCTATGGCTTCTTGGCGGAGATGCCCGCTTTGCAAAAATCTGCGCCGATCACCATCTC 303

Qy 532 ACTTTTATTGGCCCAACCCCGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGC---G 588

Db 304 ACCTTTATTGGCCCGCCAGCCCGGATTCGATTTCGAGCCATGGCGGATAAATCCACCGCTAAG 363

Qy 589 GTAACCGCCGGAAGAGGCTGCTGCCAGTTTGGCGGAATCCACCCCGAGCAAAAC 648

Db 364 GAAACAATGACGCGGTCGCGGTTCCGACGATTCCGGGCGAGTACGGTCTGCTGACGGAT 423

Qy 649 ATCGATGAGATCGTTAAAGCGCTGAAGGCCAGATTTACCCCATCTTTGTGAAGGCAGTT 708

Db 424 GTTGATTCGGCTGCCAAAGTTGCTGCCGAGATCGGCTATCCGTCATGATCAAGCGACG 483

Qy 709 GCGGTGTGGCGGACGCGGTATGCGTTTGTGTTTCACTGATGAGCTTCGCAAAATTA 768

Db 484 GCGGGGGCGGTGTTGCGGTATGCGGCTGGTGGTGCGTGACCTGCGAGATCTGAAAAAATG 543

Qy 769 GCAACAGAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGGTATGATGCGAA 828

Db 544 TTCTTTGTCGCGCAAGGAGAGCGGAGGCGGCTTTTGGGAATCCAGGACTGTATCTCGAA 603

Qy 829 CGTGTGTGATTAAACCTCAGCATATTTGAAGTGCAGATCTTGGCGATCACACTGGAGAA 888

Db 604 AAATTTATCGATCGCCCGCCAGCTTGAATTCAGATCTTGGCCGATGCTACGGCAAT 663

Qy 889 GTTGTACACCTTTATGAACGTGACTGCTCACTGCGGCTCGTCCACCAAAAGTTGTGCGAA 948

Db 664 GTAGTGCATCTAGCGAGCGGCGATTGCTCCATTCAACGTCGTCACCAAAAGCTGCTCGAA 723

Qy 949 ATTGCGCCAGCAGCATTTTGGATCCAGAACTGCGTATCGCATTTGTGCGGATGCGAGTA 1008

Db 724 GAAGCCCCAGTCCGGCGCTATCGGCGAGACCTGCGGCGAGAAATGGCGATGCGCGCGTC 783

Qy 1009 AAGTTCTGCGCTCCATTGGTTACGAGGCGCGGGAACCGTGAATTTTGTGCGATGAA 1068

Db 784 AAAGTCGCTCAAGCGATCGGCTACATCGGTGCGGCGCCGCGAGTTTCTGTCGATGCG 843

Qy 1069 AAGGGCAACACGCTTTTCATCGAAATGAACCCACGATCCAGTTGAGCACACCGTGACT 1128

Db 844 ACCGGCAACTTCTACTTCTATGGAGATGAATACCCGCTATCCCAAGTCGAGCATCCAGTCACA 903

Qy 1129 GAAGAAGTACCGAGGTGGACCTGGTGAAGCGGCAGATCGCTTGGCTGTGCTGCAACC 1188

Db 904 GAAATGATTACGGGACTGGACTTGTATGCGGAGCAGATTCCGATTGCCAAGGCG----- 958

Qy 1189 TTGAAGGAATTGGGTCTGACCCCAAGATAAGATCAAGACCCAGGTGCAGCACTGCAGTGC 1248

Db 959 ----AAGCGCTGCGCTTCCGGCAAGCCGATATTCAACTGCGGCGCCATCGATCGAATGC 1014

Qy 1249 CGCATCACCGAAGATCCAAACACCGGCTTCGCGCCAGATACCGGAACATATCACCGCG 1308

Db 1015 CGTATCAATGCGAAGATCCGGAATACAATTTCCGGCCGAAATCCTGGCCGATACAGGC 1074

Qy 1309 TACCGCTCACAGCGGAGCTGGGTTCTTGTGACGGTGCAGCTCAGCTCGGTGGCGAA 1368

Db 1075 TATTTACCGCCCGCGGCGCCCGGCTTCTGTCGATTCCCATGTTTATACCGACTACGAA 1134

Qy 1369 ATCACCGCACATTTGACTCCATCTGTTGAAATGACCTGCCGTGTTCCGACTTTGAA 1428

Db 1135 ATTCCGCCCTATTACGATTTCGCTGATTGGCAAAATTGATTCTGGGGTGCAACACGGGAA 1194

Qy 1429 ACTGCTGTTGCTCGTCACAGCGCGCTTGGCTGAGTTTCCAGTCTGCTGTTGCAACC 1488

Db 1195 GAGGCGATCGCGCGATGACGCTGCTTCGCGGAATGCGCATACCGGCTTCCGACG 1254

Qy 1489 AACATTGGTTTCTTGGCTGCTGTTGCTGCGGGAAGAGGACTTCACTTCCAGCGCATCGCC 1548

Db 1255 ACCCTTAGTTTCCATCAGCTGATGTTGAGATGCTGAGTTCTTCCGCGGGAACCTCTAT 1314

Qy 1549 ACCGGATTCAATG 1561

Db 1315 ACCAACTTTGTTG 1327

RESULT 13

US-08-485-607-5

Sequence 5, Application US/08485607

Patent No. 5792627

GENERAL INFORMATION:

APPLICANT: Robert Haselkorn and Piotr Gornicki

TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA

TITLE OF INVENTION: Carboxylase

NUMBER OF SEQUENCES: 116

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: 321 No. 5792627th Clark Street

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60610

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,607

FILING DATE: 07-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/956,700

FILING DATE: 10/21/92

ATTORNEY/AGENT INFORMATION:

NAME: Thomas E. No. 5792627thrup

REGISTRATION NUMBER: 33,268

REFERENCE/DOCKET NUMBER: ARCD:058

TELECOMMUNICATION INFORMATION:

TELEPHONE: 1-312-744-0090

TELEFAX: 1-312-755-4489

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1362 base pairs

TYPE: Nucleic acid

STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Oligonucleotide
US-08-485-607-5

Query Match 8.6%; Score 313; DB 1; Length 1362;
Best Local Similarity 53.9%; Pred. No. 5.7e-79;
Matches 718; Conservative 0; Mismatches 600; Indels 15; Gaps 3;

QY	232	TTCAAAAAGATCTTGGTAGCAAAACCGCGGCGAAATCGCGTCCGCTTCCGTCAGCA	291
Db	7	TTCAACAAGATCCTGATCGCCAATCGCGGCGAAATCGCCCTGCGCATCTCCGCACTTGT	66
QY	292	CTCGAAACCGGTGACCCACGGTAGCTATTATACCCCGTGAAGATCGGGGATCATTTCCAC	351
Db	67	CAAGAACTCGGGATCGGACGATCGCCGTTCACTCCACTGTGGATCGCAACCGGCTCCAT	126
QY	352	CGCTCTTTTGTCTGAAGCTGTCCGCAATTTGGTACCGAAGGCTCACCAGTCAAGGCGTAC	411
Db	127	GTGCAGTTAGCGGACGAAGCGGTCTGTATTGG---CGAAGCGGCCAGCAGCAAAAGCTAT	183
QY	412	CTGGACATCGATGAATATTATCGGTGACGCTAATAAAGTTAAAGCAGATGCCATTTACCCG	471
Db	184	CTCAATATCCCAACATCATTTGCGGCGCCCTGACCCCTAATGCCAGCGCCATTCACCCC	243
QY	472	GGATACGGCTTCTGTCTGAATAATGCCAGCTTGCCTCCGCGAGTGTGCGGAAACGGCAT	531
Db	244	GGCTATGGCTTCTTGGCGGAGAAATGCCCGCTTTCAGAAATCTGCGCGCATCACCATCTC	303
QY	532	ACTTTTATTGGCCCAACCCAGAGGTTCTTGAATCTCACCGGTGATAAGTCTCGCGC---G	588
Db	304	ACCTTTATTGGCCCCCAGCCCCGATTTCGATTCAGGCCATGGGCGATAAATCCACCGCTAAG	363
QY	589	GTAACCGCCGCGAAGAGGCTGTCTGCCAGTTTGGCGGAATCCACCCGAGCAAAAC	648
Db	364	GAACAATATGACGCGGTGCGGCTTCCGACGATTCGGGCGAGTGACGGTCTGTGACGGAT	423
QY	649	ATCGATGAGATCGTTAAAGCGCTGAAGCGCAGACTTACCCCATCTTTGTGAAGGCGATT	708
Db	424	GTTGATTCGGCTGCCAAAGTTGCTGCCGAGATCGGCTATCCCGTCATGATCAAAAGCGACG	483
QY	709	GCCGGTGTGGCGGACGCGGTATGCGTTTGTGCTTACCTGATGAGTTTCGCAATTA	768
Db	484	GCGGGGCGGTGTGCGCGTATGCGGTGTGCGTGACCTGACCTGCGATCTGGAATACTG	543
QY	769	GCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGGCTATATGCGAA	828
Db	544	TTCCTTGTGCTGCCAAGGAGAGCGGAGGCGAGCTTTTGGGAATCCAGGACTGATCTCGAA	603
QY	829	CGTGTGTGATTAAACCTCAGCATATTGAAGTCAGATCCTTGGCGATCACACTGGAGAA	888
Db	604	AAATTTATCGATCGCCACGCCACGTTGAATTTAGATCTTGGCGGATGCTACGGCAAT	663
QY	889	GTTGTACACCTTTATGAACGTGACTGCTCAGTCAGCGTCTGTCACCAAAAAGTTGTCGAA	948
Db	664	GTAGTGATCTAGCGGAGCGGATGCTCTCAATTCACAGTCTGTCACCAAAAAGCTGTCGAA	723
QY	949	ATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGTGATCGCATTTTGGCGGATGCAGTA	1008
Db	724	GAAGCCCCCAGTCCGCGCTATCGGCAGACCTGCGGCAGAAATGGGCGATGCCGCGTC	783
QY	1009	AAGTTCTGCGCTCCATTGGTTACCGGGCGGCGGAAACCGTGAATTTCTTGTGATGAA	1068
Db	784	AAAGTCGCTCAAGCGATCGGCTACATCGTTCGCGGCACCGTGGAGTTTCTGTCGATCGG	843
QY	1069	AAGGGCAACCACTTTCATCGAAATGAACCCAGTATCCAGTTGAGCAGCACCCGTGACT	1128
Db	844	ACCGGCAACTTCTACTTTCATGGAGATGAATACCCGCATCCAAAGTCGAGCATCCAGTCACA	903
QY	1129	GAAGAAGTCACCGAGGTGACCTGTTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACC	1188
Db	904	GAAATGATTACGGGACTGGACTTGTATTGCGGAGCAGATTCGGATTGCCCAAGCGC----	958

QY	1189	TTGAAGGAATTGGTCTGACCCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGC	1248
Db	959	----AAGCGTGGCTTCCGGCAAGCCGATATTCAACTGGCGGCGCATCGATCGAATGC	1014
QY	1249	CGCATCACCAACGGAAGATCCAAACAAACGGCTTCCGCCAGATACCGGAACATATCACCGCG	1308
Db	1015	CGTATCAATGCGGAAGATCCGGAATACAATTTCCGCCGAATCTTGGCCGATACAGGC	1074
QY	1309	TACCGTTCACAGCGGAGCTGGCGTTCTGCTTGAACGGTGCAGTCCAGTCCGTTGCGAA	1368
Db	1075	TATTTACCGCCCGCGGCCCGCGCTTCTGTCGATTCCCATGTTTATACCGACTACGAA	1134
QY	1369	ATCACCGCACACTTTGACTCCATGCTGTTGAAATGACCTGCCGTTGTTCCGACTTTGAA	1428
Db	1135	ATTCCGCCCTATTACGATTGCTGATTGGCAAAATTGATTGTTGGGTGCAACACGGGAA	1194
QY	1429	ACTGCTGTTGCTGTCGTCACAGCGCGGTTGGCTGAGTTCAACCGTGTGTTGTTGCAACC	1488
Db	1195	GAGCGATCGCGCGGATGACGCTGCTTGGCGGAATGCGCCATCACCGGCTTGCAGCG	1254
QY	1489	AACATTGTTTCTGCTGCTGCTGCTGCGGGAAGAGGACTTCACTTCCAAAGCGCATCGCC	1548
Db	1255	ACCTTAGTTTCCATCAGTGTGTTGCAATGCTGAGTTCCTGCGGGGAATCTCTAT	1314
QY	1549	ACCGGATTTCATTG	1561
Db	1315	ACCAACTTTGTTG	1327

RESULT 14

US-08-475-879-5
; Sequence 5, Application US/08475879
; Patent No. 5972644
; Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5972644 5786170th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1362 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Oligonucleotide
US-08-475-879-5

Search completed: March 23, 2004, 18:39:49
Job time : 257 secB

QY	532	ACTTTTATGGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGC---G	588
Db	304	ACCTTTATGGCCCCAGCCCGGATTCGATTCGAGCCATGGGCGATAAATCCACCGCTAAG	363
QY	589	GTAACCGCGCGAAGAGGCTGGTCTGCCAGTTTGGCGGAATCCACCCGAGCAAAAAC	648
Db	364	GAACAATGAGCGGGTCGGGTTCCGACGATTCGGGGCAGTACGGTCTGCTGACGGAT	423
QY	649	ATCGATGAGATCGTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTT	708
Db	424	GTTGATTCGGCTGCCAAAGTTGCTGCGAGATCGGCTATCCCGTCATGATCAAAGCGACG	483
QY	709	GCCGGTGGTGGCGGACGCGGTATGCGTTTGTGTTTCACTGATGAGCTTCGCAATTA	768
Db	484	GCGGGGGCGGTGCGGTTATGCGGTGCGTGGTGGTGACCTGCAGATCTGAAAAAATG	543
QY	769	GCAACAGAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGGTATATGCGAA	828
Db	544	TTCCCTTGTGTCCAAGGAGAGCGCGAGCAGCTTTTGGGAATCCAGGACTGTATCTCGAA	603
QY	829	CGTGTGTGATTAACCCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAA	888
Db	604	AAATTTATCGATCGCCACGCCACGTTGAATTCAGATCTTGGCCGATGCCTACGSCAAT	663
QY	889	GTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCTGCACCAAAAAGTTGCGAA	948
Db	664	GTAGTGATCTAGCGAGCGCGATTGTCTCAATCAACGTCTGCACCAAAAAGCTGCTCGAA	723
QY	949	ATTGCGCCAGCAGCAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTA	1008
Db	724	GAAGCCCCCAGTCCGGCGCTATCGGCAGACCTCGGCAGAAAATGGCGATGCCGCCGTC	783
QY	1009	AAGTTCTGCCGCTCCATTGTTACCAAGGCGCGGAACCGTGAATCTTTGGTCGATGAA	1068
Db	784	AAAGTCGCTCAAGCGATCGGCTACATCGGTGCCGACCCGTGGAGTTTCTGGTCGATGCG	843
QY	1069	AAGGGCAACACGCTTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACT	1128
Db	844	ACCGGCAACTTCTACTTCATGGAGATGAATACCCGCATCCAAGTCGAGCATCCAGTCACA	903
QY	1129	GAAGAAGTCACCGAGGTGGACCTGGTGAAGCGGCAGATGCGCTTGGCTGCTGGTGCAACC	1188
Db	904	GAATGATTACGGGACTGGACTTGATTGCGGAGCAGATTCCGATTCGCCAAGGCG-----	958
QY	1189	TTGAAGGAATTGGGTCTGACCCAGATAAGATCAAGACCCACGGTGCAGCAGTGCAGTGC	1248
Db	959	----AAGCGCTGCGCTTCCGGCAAGCCGATATTCAACTGCGCGGCCATGCGATCGAATGC	1014
QY	1249	CGCATCACCAAGGAATCCAAACAACGGCTTCCGCCAGATACCGGAACCTATCACCGCG	1308
Db	1015	CGTATCAATGCGGAAGATCCGGAATACAAATTCGGGCCGAATCCTGGCCGCATTACAGGC	1074
QY	1309	TACCGCTCACAGCGGAGCTGGCGTTGCTTGACGGTGCAGTGCAGTCCGTTCCGACTTTGAA	1368
Db	1075	TATTTACCGCCCGCGGCCCGCGCTTCGTGTCGATTCCCATGTTTATACCGACTACGAA	1134
QY	1369	ATCACCGCACACTTTGACTCCATGCTGGTGAATAATGACCTGCCGTGGTCCGACTTTGAA	1428
Db	1135	ATTCCGCCCTATTACGATTGCTGATTGGCAAAATTGATTGTCTGGGTGCAACACGGGAA	1194
QY	1429	ACTGCTGTTGCTGTCAGACAGCGCGCTTGGCTGAGTTTCAACCGTGTCTGGTGTGCAACC	1488
Db	1195	GAGCGGATCGCGCGGATGCAGCGTCTCTGCGGAATGCGCCATCACCAGCTTGGCCGACG	1254
QY	1489	AACATTGGTTTCTTGCCTGCGTGTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCC	1548
Db	1255	ACCCTTAGTTTCCATCAGCTGATGTTGCAGATGCTGAGTTTCTGCGGGGGAACCTCTAT	1314
QY	1549	ACCGGATTCAATG	1561
Db	1315	ACCAACTTTGTTG	1327

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run-on: March 23, 2004, 20:24:42 ; Search time 1213 Seconds
(without alignments)
11042.568 Million cell updates/sec

Title: US-10-045-072-1
Perfect score: 3621
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3621	100.0	3621	14	US-10-045-072-1	Sequence 1, Appli
2	3621	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
3	3420	94.4	3420	9	US-09-738-626-765	Sequence 765, App
4	3398.8	93.9	3474	9	US-09-974-973-1	Sequence 1, Appli
5	3398.8	93.9	3474	9	US-09-974-973-3	Sequence 3, Appli
6	1927.4	53.2	3423	12	US-10-282-122A-17701	Sequence 17701, A
7	1361.6	37.6	3381	12	US-10-282-122A-25766	Sequence 25766, A
8	1294.4	35.7	3384	12	US-10-282-122A-28626	Sequence 28626, A
9	1292.2	35.7	3381	12	US-10-282-122A-26500	Sequence 26500, A
10	681	18.8	3945	9	US-09-917-800A-1566	Sequence 1566, Ap
11	677.4	18.7	4017	9	US-09-880-107-3029	Sequence 3029, Ap
12	659	18.2	3432	15	US-10-369-493-31453	Sequence 31453, A
13	643.6	17.8	3459	15	US-10-369-493-35714	Sequence 35714, A
14	617	17.0	3441	15	US-10-369-493-35137	Sequence 35137, A
15	617	17.0	3453	15	US-10-369-493-38504	Sequence 38504, A

16	617	17.0	3453	15	US-10-369-493-38693	Sequence 38693, A
17	601.8	16.6	3453	15	US-10-369-493-41025	Sequence 41025, A
18	598	16.5	4152	15	US-10-398-221-3692	Sequence 3692, Ap
19	582	16.1	3414	15	US-10-369-493-42038	Sequence 42038, A
20	577.2	15.9	3441	12	US-10-282-122A-24304	Sequence 24304, A
21	572.8	15.8	3447	15	US-10-369-493-46799	Sequence 46799, A
22	565.2	15.6	3537	15	US-10-369-493-45626	Sequence 45626, A
23	565	15.6	1163020	15	US-10-398-221-10	Sequence 10, Appli
24	565	15.6	3011208	15	US-10-398-221-2058	Sequence 2058, Ap
25	549.4	15.2	3540	15	US-10-369-493-25178	Sequence 25178, A
26	548.8	15.2	3501	15	US-10-369-493-46506	Sequence 46506, A
27	548.8	15.2	3555	15	US-10-369-493-26175	Sequence 26175, A
28	547.2	15.1	2709	15	US-10-369-493-37987	Sequence 37987, A
29	522	14.4	3444	12	US-10-282-122A-10682	Sequence 10682, A
30	514	14.2	3429	9	US-09-815-242-6709	Sequence 6709, Ap
31	509.2	14.1	3426	12	US-10-282-122A-6344	Sequence 6344, Ap
32	500.4	13.8	20072	9	US-09-070-927A-89	Sequence 89, Appli
33	482.4	13.3	3426	12	US-10-282-122A-21758	Sequence 21758, A
34	479.8	13.3	5030	8	US-08-781-986A-324	Sequence 324, App
35	479.8	13.3	5030	12	US-10-329-624-324	Sequence 324, App
36	479.6	13.2	3453	12	US-10-282-122A-8207	Sequence 8207, Ap
37	478.2	13.2	3441	9	US-09-815-242-4413	Sequence 4413, Ap
38	462.6	12.8	3435	12	US-10-282-122A-15904	Sequence 15904, A
39	449.4	12.4	3432	12	US-10-282-122A-16593	Sequence 16593, A
40	421.8	11.6	3222	9	US-09-815-242-8263	Sequence 8263, Ap
41	420.6	11.6	3429	12	US-10-282-122A-16733	Sequence 16733, A
42	363.8	10.0	1362	15	US-10-369-493-36893	Sequence 36893, A
43	358.4	9.9	3230	15	US-10-369-493-37518	Sequence 37518, A
44	337.2	9.3	4161	15	US-10-369-493-27492	Sequence 27492, A
45	311.4	8.6	1362	9	US-09-767-479-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-045-072-1
; Sequence 1, Application US/10045072
; Publication No. US20030027305A1
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790002
; CURRENT APPLICATION NUMBER: US/10/045,072
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 09/677,575
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 09/220,081
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(3621)
US-10-045-072-1

Query Match 100.0%; Score 3621; DB 14; Length 3621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TGGGGCGGGGTTAGATCCTGGGGGTTATTTCATTCACTTTGGCTTGAAGTCGTCAGG	60
Db	1	TGGGGCGGGGTTAGATCCTGGGGGTTATTTCATTCACTTTGGCTTGAAGTCGTCAGG	60
QY	61	TCAGGGGAGTGTGCCCGAAAAACATTGAGAGAAAAACAAACCGATGTTTATTTGGGGG	120
Db	61	TCAGGGGAGTGTGCCCGAAAAACATTGAGAGAAAAACAAACCGATGTTTATTTGGGGG	120

QY 121 AATCGGGGTTACGATACCTAGGACGAGTGAATGCTATCAACCTTGGCGGTCTCTTTGTTG 180
Db 121 AATCGGGGTTACGATACCTAGGACGAGTGAATGCTATCAACCTTGGCGGTCTCTTTGTTG 180
QY 181 AAAGGAATAATTAATCTAGTGTGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
Db 181 AAAGGAATAATTAATCTAGTGTGACTCACACATCTTCAACGCTTCCAGCATTCAAAAAG 240
QY 241 ATCTTGGTAGCAAAACCGCGGCGAAATCGCGGTCCGTCTTTCCGTGACACCTCGAAACC 300
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QY 301 GGTGACGCCACGGTAGCTATTTACCCCGTGAAGATCGGGGATCAATCCACCGCTCTTTT 360
Db 301 GGTGACGCCACGGTAGCTATTTACCCCGTGAAGATCGGGGATCAATCCACCGCTCTTTT 360
QY 361 GCTTCTGAAGCTGTCCGATTTGGTACCGAAGGCTCACAGTCAAGGCGTACCTGGACATC 420
Db 361 GCTTCTGAAGCTGTCCGATTTGGTACCGAAGGCTCACAGTCAAGGCGTACCTGGACATC 420
QY 421 GATGAAATTAATCGGTGAGCTAAAAAGTTAAAGCAGATGCCATTTACCCGGGATACGGC 480
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Db 1141 GAGGTGACCTGGTGAAGGCGGAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200

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Db 1741 CGCCTGAAGCAGCTTGGCCAGCGCGTGTGCTGCTGATCTCCGTGAGCAGGACGCACCTG 1800
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Db 1801 GCAGTTACTGATACCACTTCCGCGATGCACACCACTCTTTGCTTGGACCCGAGTCCGC 1860
QY 1861 TCATTCCGACTGAAGCCTGCGGCAGAGGCGCTGCAAGCTGACTCCTGAGCTTTTGTCC 1920
Db 1861 TCATTCCGACTGAAGCCTGCGGCAGAGGCGCTGCAAGCTGACTCCTGAGCTTTTGTCC 1920
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Db 1921 GTGAGGCTTGGGCGGCGGACCTACGATGTGGCGATCGCTTCTCTTGGAGGATCCG 1980
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QY 2521 ACCACCTCCAGCCATCCCTGTCTGCCATTGTTGCTGCAATTCGCGCACACCGTTCGCGAT 2580
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QY 2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCACTGCGCGGA 2640
Db 2581 ACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCACTGCGCGGA 2640
QY 2641 CTGTACTGCTCCATTGAGTCTGGAACCCAGGCCCAACCGGTGCGTCTACCGCCACGAA 2700
Db 2641 CTGTACTGCTCCATTGAGTCTGGAACCCAGGCCCAACCGGTGCGTCTACCGCCACGAA 2700
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Db 2761 CGTTTCGAACTCATCGAAGACAACTACGACGCGGTTAATGAGATGCTGGGACGCCCAACC 2820
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Db 2941 GCGTTCCTGCGCGCGAGCTTGTTAAACCTCCAGGTGGTGGCCAGAGCCACTGCGCAC 3000
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QY 3121 TTCCCGAAGCCAAACCGAAGAGTTCTTCGAGCAACCGTTCGCGCAACACCTCTGCG 3180
Db 3121 TTCCCGAAGCCAAACCGAAGAGTTCTTCGAGCAACCGTTCGCGCAACACCTCTGCG 3180
QY 3181 CTGGATGATCGTGAATTTCTTACGGCCTGGTCCGAAGCCGCGAGACTTTGATCCGCGCTG 3240
Db 3181 CTGGATGATCGTGAATTTCTTACGGCCTGGTCCGAAGCCGCGAGACTTTGATCCGCGCTG 3240
QY 3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCTGATGCGATCTCTGAGCCAGACGATAAG 3300
Db 3241 CCAGATGTGCGCACCCCACTGCTTGTTCGCTGATGCGATCTCTGAGCCAGACGATAAG 3300
QY 3301 GGTATGCGCAATGTTGTGGCAACGTCACCGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
Db 3301 GGTATGCGCAATGTTGTGGCAACGTCACCGGCCAGATCCGCCCAATGCGTGTGCGTGAC 3360
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Db 3421 GTTGCTGCACCATTCGCTGGTGTGTGTCAACCGTCACTGTTGCTGAAGGTGATGAGGTCAAG 3480
QY 3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACATCACTGCTTCT 3540
Db 3481 GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACATCACTGCTTCT 3540
QY 3541 GTTGACGGCAAAATCGATCGCGTGTGTGTTCTCTGCTCAACGAAGGTGGAAGTGGCGGAC 3600
Db 3541 GTTGACGGCAAAATCGATCGCGTGTGTGTTCTCTGCTCAACGAAGGTGGAAGTGGCGGAC 3600
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Db 3601 TTGATCGTCTGCTGTTTCTCTAA 3621

RESULT 2
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 100.0%; Score 3621; DB 9; Length 3309400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGGGCGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 60
Db 705013 TGGGGCGGGTTAGATCCTGGGGGGTTTATTTCATTCACTTTGGCTTGAAGTCGTGCAGG 705072
QY 61 TCAGGGGAGTGTTCGCCGAAACATTGAGAGGAAACAAAAACCGATGTTGATTTGGGG 120
Db 705073 TCAGGGGAGTGTTCGCCGAAACATTGAGAGGAAACAAAAACCGATGTTGATTTGGGG 705132
QY 121 AATCGGGGGTTACGATACTAGGACGCGAGTGTCTGCTATCACCCCTTGGCGGTCTCTTTG 180
Db 705133 AATCGGGGGTTACGATACTAGGACGCGAGTGTCTGCTATCACCCCTTGGCGGTCTCTTTG 705192
QY 181 AAAGGAATAATTACTCTAGTGTGACTCACAATCTTCAACGCTTCCAGCATTTCAAAAAG 240
Db 705193 AAAGGAATAATTACTCTAGTGTGACTCACAATCTTCAACGCTTCCAGCATTTCAAAAAG 705252
QY 241 ATCTTGGTAGCAAAACCGCGCGAAATCGCGGTCCGTGCTTTCCGTGACGACTCGGAAACC 300

Db 705253 ATCTTGGTAGCAACCGCGGAAATCGCGGTCCGTGCTTTCCGTGCAGCACTCGAAACC 705312
QY 301 GGTGCAGCCACGGTAGCTATTTACCCCGGTGAAGATCGGGATCAFTCCACCGCTCTTTT 360
Db 705313 GGTGCAGCCACGGTAGCTATTTACCCCGGTGAAGATCGGGATCAFTCCACCGCTCTTTT 705372
QY 361 GCTTCTGAAGCTGTCGGTATGGTACCGAAGGCTCACCAAGTCAAGGGTACCTGGACATC 420
Db 705373 GCTTCTGAAGCTGTCGGTATGGTACCGAAGGCTCACCAAGTCAAGGGTACCTGGACATC 705432
QY 421 GATGAAATTATCGGTGCAGCTTAAAGGTTAAAGCAGATGCCATTTACCCCGGATACGGC 480
Db 705433 GATGAAATTATCGGTGCAGCTTAAAGGTTAAAGCAGATGCCATTTACCCCGGATACGGC 705492
QY 481 TTCCTGTCTGAAATGCCAGCTTGCCCGGAGTGTGCGGAAACCGCATTTACTTTTATT 540
Db 705493 TTCCTGTCTGAAATGCCAGCTTGCCCGGAGTGTGCGGAAACCGCATTTACTTTTATT 705552
QY 541 GGCCCAACCCAGAGGTTCTTGATCTCACCCGGTGATAAGTCTCGCGGCTAACCCCGCG 600
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Db 705613 AAGAAGGCTGGTCTGCCAGTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAGATC 705672
QY 661 GTTAAAAAGCGTGAAGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCGGTTGGTGGC 720
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Db 706093 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCAACACCGTGACTGAAGAGTCAAC 706152
QY 1141 GAGGTGACCTGGTGAAGGGCGAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 1200
Db 706153 GAGGTGACCTGGTGAAGGGCGAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTG 706212
QY 1201 GGTCTACCCAAAGATAAGATCAAGACCCACGGTGAGCACTGCAGTCCCGCATCACCA 1260
Db 706213 GGTCTACCCAAAGATAAGATCAAGACCCACGGTGAGCACTGCAGTCCCGCATCACCA 706272
QY 1261 GAAGATCCAAACAAACGGCTTCCGCCAGATACCGGAATATACCCGGTACCGCTCACCA 1320
Db 706273 GAAGATCCAAACAAACGGCTTCCGCCAGATACCGGAATATACCCGGTACCGCTCACCA 706332
QY 1321 GCGGAGTGGCGTTTGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCAC 1380

Db 706333 GCGGAGCTGCGGTTCTGTTGACGGTGCAGCTCAGCTCGGTGGCGAAATCACCGCAC 706392
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Db 706393 TTTGACTCCATGCTGGTGAAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTTGCT 706452
QY 1441 CGTGACAGCGCGGTTGGCTGAGTTCAACCGTGTCTGGTGTGCAACCAACATTGGTTTC 1500
Db 706453 CGTGACAGCGCGGTTGGCTGAGTTCAACCGTGTCTGGTGTGCAACCAACATTGGTTTC 706512
QY 1501 TTGCGTGGCTTGTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTCATT 1560
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QY 1621 GATTACTTGGCAGATGTACCGTGAACAAGCCTCATGGTGTGCGTCCAAAAGGATGTTGCA 1680
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QY 1981 TGGACAGGCTCGACGAGCTGCGGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTT 2040
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707893 GTGGATCCAGCAGACTTGTGTCGGATCCACAAAGTACGACATCCAGACTCTGTCTATC 707952
QY |||||
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707953 GCGTTCCTGCGCGGAGCTTGTTAACCTCCAGGTGGTGGTGGCCAGAGCCACTGCGCACC 708012
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708013 CGCGCACTGGAAGCGCGCTCCGAAGGCAAGGCACTCTGACGGAAGTTCCTGAGGAAGAG 708072
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708133 TTCCCGAAGCCAAACCGAAGAGTTCCTCGAGCAACCGTCCCGCTTCGGCAACACCTCTGCG 708192
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Db |||||
708193 CTGGATGATCGTGAATCTTCTACGGCTGTGTCGAAGCCCGCGAGACTTTGATCCGCTG 708252
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708253 CCAGATGTGCGCACCCCACTGCTTGTTCGCTGGATGCGATCTCTGAGCCAGACGATAAG 708312
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708313 GGTATGCGCAATGTTGTGGCCAAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGTGAC 708372
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3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAGGCAGATTCTCTCAACAAGGGCCAT 3420
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708433 GTTGTGCACCAATCGCTGGTGTGTACCGTGACTGTGTGTAAGGTGATGAGGTCAAG 708492
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RESULT 3
US-09-738-626-765
; Sequence 765, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 765
; LENGTH: 3420
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-765

Query Match 94.4%; Score 3420; DB 9; Length 3420;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 379 ATTGGTACCGAAGGCTCACCAAGTCAAGGCGTACCTGGACATCGATGAAATTCGGTGCA 438
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QY 559 CTTGATCTCACCGGTGATAAGTCTCGCGCGGTAAACCGCCGGAAGAGGCTGCTGTGCCA 618
Db 361 CTTGATCTCACCGGTGATAAGTCTCGCGCGGTAAACCGCCGGAAGAGGCTGCTGTGCCA 420

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Qy 3559 CGCGTTGTGTTCTGCTGCAACGAAGGTGGAAGGTGCGGACTTGAATCGTCTGTTTCC 3618
Db 3361 CGCGTTGTGTTCTGCTGCAACGAAGGTGGAAGGTGCGGACTTGAATCGTCTGTTTCC 3420

RESULT 4
US-09-974-973-1
; Sequence 1, Application US/09974973
; Patent No. US2002017202A1
; GENERAL INFORMATION:
; APPLICANT: Hanke, Paul D.
; TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacterium
; FILE REFERENCE: 1533.1230001/MAC/RGM
; CURRENT APPLICATION NUMBER: US/09/974,973
; CURRENT FILING DATE: 2001-10-21
; PRIOR APPLICATION NUMBER: US 60/239,913
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3474
; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (3474)
US-09-974-973-1
Query Match 93.9%; Score 3398.8; DB 9; Length 3474;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 3427; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
Qy 148 GTGACTGCTATCACCCCTTGGCGGTCTCTTGTGTTGAAAGGAATAATTAATCTAGTGTGCGACT 207
Db 1 GTGACTGCTATCACCCCTTGGCGGTCTCTTGTGTTGAAAGGAATAATTAATCTAGTGTGCGACT 60
Qy 208 CACACATCTTCAACGCTTCCAGCATTCAAAAGATCTTGGTAGCAAAACCGCGGCGGAAATC 267
Db 61 CACACATCTTCAACGCTTCCAGCATTCAAAAGATCTTGGTAGCAAAACCGCGGCGGAAATC 120
Qy 268 GCGGTCCGTGCTTCCGTGCGACACTCGAAACCGGTGCGACGACCGTAGCTATTTACCCC 327
Db 121 GCGGTCCGTGCTTCCGTGCGACACTCGAAACCGGTGCGACGACCGTAGCTATTTACCCC 180
Qy 328 CGTGAAGATCGGGGATCATTCACCGCTCTTTTGTCTTCTGAAGTGTCCGCATTTGGTACC 387
Db 181 CGTGAAGATCGGGGATCATTCACCGCTCTTTTGTCTTCTGAAGTGTCCGCATTTGGTACC 240
Qy 388 GAAGGCTCACAGTCAAGCGGTACTCTGGACATCGATGAATAATATCGGTGCAGCTAAAAA 447
Db 241 GAAGGCTCACAGTCAAGCGGTACTCTGGACATCGATGAATAATATCGGTGCAGCTAAAAA 300
Qy 448 GTTAAAGCAGATGCCATTTACCCGGGATACCGCGGCGAAGAGGCTGTGTTGAGTCTTGC 507
Db 301 GTTAAAGCAGATGCCATTTACCCGGGATATGGCTTCTGTCTGAAAAATGCCAGCTTGCC 360
Qy 508 CGCGAGTGTGCGGAAAAACGGCATTAATTTTATTTGGCCCCAACCCAGAGGTTCTTGATCTC 567
Db 361 CGCGAGTGTGCGGAAAAACGGCATTAATTTTATTTGGCCCCAACCCAGAGGTTCTTGATCTC 420
Qy 568 ACCGTTGATAAGTCTCGCGGTAACCGCGGCGAAGAGGCTGTGTTGAGTCTTGCAGTTTGGCG 627
Db 421 ACCGTTGATAAGTCTCGCGTAAACCGCGGCGAAGAGGCTGTGTTGAGTCTTGCAGTTTGGCG 480
Qy 628 GAATCCACCCCGAGCAAAACATCGATGAGATCGTTAAAGCGTGAAGGCCAGACTTAC 687
Db 481 GAATCCACCCCGAGCAAAACATCGATGAGATCGTTAAAGCGTGAAGGCCAGACTTAC 540
Qy 688 CCCATCTTTGTAAGGCGAGTTGCCGTTGGCGGACGCGGTATGCGTTTGTGTTCTTCA 747
Db 541 CCCATCTTTGTAAGGCGAGTTGCCGTTGGCGGACGCGGTATGCGTTTGTGTTCTTCA 600
Qy 748 CCTGATGAGCTTCGCAAAATAGCAACAGAGCATCTCGTGAAGTGAAGCGGCTTTCGGC 807
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Qy 808 GATGCGCGGTATATGTCGAACGTCGTGTGATTAACCCCTCAGCATATTGAAGTGCAGATC 867
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Qy 868 CTTGGCGATCACACTGGAGAAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT 927
Db 721 CTTGGCGATCGCACTGGAGAAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT 780
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Db 781 CGTCACCAAAAAGTTGCGAAATTTGCGCCAGCAAGCATTTGGATCCAGAACTGCGTGTAT 840
Qy 988 CGCATTTGTGCGGATGAGTAAAGTTCTGCGGCTCCATTTGTTACCGAGGCGGCGGAAACC 1047
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Qy 1048 GTGGAATTTCTTGGTTCGATGAAAGGGCAACCGTCTTTCATCGAAATGAACCCAGCTATC 1107
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Db 3121 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAAGTC 3180
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Db 3181 AACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCAACCGCAACC 3240
QY 3388 GCAGAAAAGGAGATTCCTCCAAACAAAGGGCCATGTTGCTGCACCATTCGCTGGTGTGTC 3447
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QY 3508 GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAAAATCGATCGCGTGTG 3567
Db 3361 GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAGATTTGAACGCGTGTG 3420
QY 3568 GTTCCTGCTGCAACGAAGGTGGAAGGTGGCGGACTTGATCGTCTGTTTCCCTAA 3621
Db 3421 GTTCCTGCTGCAACGAAGGTGGAAGGTGGCGGACTTGATCGTCTGTTTCCCTAA 3474

RESULT 5

US-09-974-973-3
; Sequence 3, Application US/09974973
; Patent No. US20020177202A1
; GENERAL INFORMATION:
; APPLICANT: Hanke, Paul D.
; TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacterium
; FILE REFERENCE: 1533.123001/MAC/RGM
; CURRENT APPLICATION NUMBER: US/09/974,973
; CURRENT FILING DATE: 2001-10-21
; PRIOR APPLICATION NUMBER: US 60/239,913
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3474
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-974-973-3

Query Match 93.9%; Score 3398.8; DB 9; Length 3474;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 3427; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 148 GTGACTGCTATCACCCCTTGGCGGTCTCTGTTGAAAGGAATAATACTCTAGTGTGACT 207
Db 1 GTGACTGCTATCACCCCTTGGCGGTCTCTGTTGAAAGGAATAATACTCTAGTGTGACT 60
QY 208 CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAAACCGCGCGAAATC 267
Db 61 CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAAACCGCGCGAAATC 120
QY 268 GCGGTCCGTGCTTTCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC 327
Db 121 GCGGTCCGTGCTTTCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC 180
QY 328 CGTGAAGATCGGGATCATTCACCCGCTCTTTGCTTCTGAAGTGTCCGCAATTGGTACC 387
Db 181 CGTGAAGATCGGGATCATTCACCCGCTCTTTGCTTCTGAAGTGTCCGCAATTGGTACT 240
QY 388 GAAGGCTCACCAAGGTCAAGGGTACCTGGACATCGATGAAATATCGGTGCAAGTAAAAA 447
Db 241 GAAGGCTCACCAAGGTCAAGGGTACCTGGACATCGATGAAATATCGGTGCAAGTAAAAA 300
QY 448 GTTAAAGCAGATGCCATTTACCCGGGATACGGCTTCTGCTGAAAAATGCCAGCTTACC 507
Db 301 GTTAAAGCAGATGCTATTTACCCGGGATATGGCTTCTGCTGAAAAATGCCAGCTTACC 360
QY 508 GCGAGTGTGCGGAAAAACGGCATTACTTTTATTTGGCCCAACCCACAGAGGTTCTTGTATCTC 567

Db 361 CGCAGTGGCGGAAAAACGGCAATTAATTTATTTGGCCCAACCCAGAGGTTCTTGTATCTC 420
QY 568 ACCGGTGATAAGTCTCGCGCGGTAAACCGCCGCGAAGAAAGGCTGGTCTGCCAGTTTTGGCG 627
Db 421 ACCGGTGATAAGTCTCGTGCCTGTAACCGCCGCGAAGAAAGGCTGGTCTGCCAGTTTTGGCG 480
QY 628 GAATCCACCCCGAGCAAAAACATCGATGAGATCGTTAAAAAGCGTGAAGGCCAGACTTAC 687
Db 481 GAATCCACCCCGAGCAAAAACATCGATGACATCGTTAAAAAGCGTGAAGGCCAGACTTAC 540
QY 688 CCCATCTTTGTGAAGGCAGTTGCCGCTGGTGGCGGACGCGGTATGCGTTTGTGCTTCA 747
Db 541 CCCATCTTTGTGAAGGCAGTTGCCGCTGGTGGCGGACGCGGTATGCGTTTGTGCTTCA 600
QY 748 CCTGATGAGCTTCGCAAAATTAGCAACAGAAAGCATCTCGTGAAGTGAAGCGGCTTTCGGC 807
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QY 808 GATGGCGCGGTATATGTGAAACGCTGTGTGATTAAACCCCTCAGCATATTGAAGTGCAGATC 867
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Db 1741 GCCGTGCGAAAGTGAATCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 1860
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Db 2521 CCAGGCCCAACCGGTCGCTTACCGGCCACGAAATCCAGGCGGACAGTGTCCAAACCTG 2580

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Db 2581 CGTGCAAGGCCCAACCGCACTGGGCTTGGGATCGTTTCGAACTCATCGAAGACAATAC 2640
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QY 2848 GCGACCTCGCACTCCACCTCGTTGGTGGGTTGATCCAGCAGACTTTGCTGCGGAT 2907
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QY 3208 CTGGTCGAAGCGCGGAGACTTTGATCCGCTGCGCAGATGTCGACCCCACTGCTTGT 3267
Db 3061 CTGGTCGAAGCGCGGAGACTTTGATCCGCTGCGCAGATGTCGACCCCACTGCTTGT 3120
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QY 3328 AACGGCCAGATCCGCGCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCAACCGCAACC 3387
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QY 3388 GCAGAAAAGGCGAGATTCCTCCAAACAAAGGGCCATGTTGTCGACCATTCGCTGGTGTGTC 3447
Db 3241 GCAGAAAAGGCGAGATTCCTCCAAACAAAGGGCCATGTTGTCGACCATTCGCTGGTGTGTC 3300
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QY 3568 GTTCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGTGATCGTCTGCTTCTCTAA 3621
Db 3421 GTTCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGTGATCGTCTGCTTCTCTAA 3474

RESULT 6

US-10-282-122A-17701
; Sequence 17701, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith

QY 1773 TCGTGATCTCCGTGAGCAGCAGCAGCAGTACTGATPACCACCTTCCGCGATGCACA 1832
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Db 1644 TCAGTGCCTTCTCGCAACCCGCGTGGCTCCAAACACGCTGATCGACGACGACGACGCT 1703
QY 1893 CGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGCCCTGGGCGGCGCGACCTACGATGT 1952
Db 1704 CGCAAAGCTCACCCAGAGCTGCTCTGTAGAAGCATGGGTGGTGTACCTATGACGT 1763
QY 1953 GCGGATGCGTTCCTCTTTGAGGATCCGCTGGGACAGGCTCGACGAGCTGCGGAGGCGAT 2012
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QY 2073 CCCGACTCCGCTGCGCGCGCTTTGTTAAGGAAGCTGCCAGCTCCGCGTGGACATCTT 2132
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QY 2133 CCGCATCTTCGACGCGCTTAACGACGCTCTCCAGATGCGTCCGCAATCGACGCGTCT 2192
Db 1944 CCGCATCTTCGACGCGCTTAACGACGCTCTCCAGATGCGTCCGCAATCGACGCGTCT 2003
QY 2193 GGAGACCAACACCGCGGTAGCCGAGGTGGTATGGCTTATTTCTGGTGTATCTCTGATCC 2252
Db 2004 CGAAACCAACACACAGATTCGCGAAGTCGAATGGCTACTCCGCTGATCTGACCAACC 2063
QY 2253 AAATGAAAAGCTCTACACCCCTGGATTACTTAAAGATGGCAGAGGAGATCGTCAAGTC 2312
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Db 2724 AAAGTACGATATTCCTGACTCCGTCTATGCTTCTTCTTCTCGTGGTGGCTCGGCACCCCTCC 2783
QY 2973 AGGTGGTGGCCAGAGCCACTGCGCACCCCGCGCACTGSAAGGCCGCTCCGAAAGGCAAGGC 3032
Db 2784 AGCGGCTGGCCAGAGAACTCGGTGCTAAGGCATTTGCGAGGACGTAAGGAATCAAAGGA 2843
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Db 2844 CACATTGCCCCGCTGCCAGCAGAGATGAAGCTCTGCTCGCAGATCGTGGCAGCC----- 2898
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Db 3318 GAAGATGGAGGCAACGATCTCTGCCACACAGACGGAACCGTCCGACCGTATCGTCTTGAC 3377
QY 3573 TGCTGCAACGAAGGTGGAAGGTGGCGACTGATCGTCTGT 3611
Db 3378 GCAGGCCACCAAGGTGGAAGGTGGAGACTGCTCTCTCGT 3416

RESULT 7

US-10-282-122A-25766
; Sequence 25766, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A


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; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25766

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US-10-282-122A-25766

	Query Match	37.6%;	Score 1361.6;	DB 12;	Length 3381;
	Best Local Similarity	63.2%;	Pred. No. 0;		
	Matches 2131;	Conservative	0;	Mismatches 1234;	Indels 9; Gaps 2;
QY	238	AAGATCTTGGTAGCAAAACCGGCGGAGAAATCGCGTCCGTGCTTTCCGTGCAGCACTCGAA	297		
DB	10	AAAGTCCTGGTCGCCAACCGGCGGAGATCGCGATCCGCGGCTTCGCGCGGCTTACGAG	69		
QY	298	ACCGGTGCAGCCACGGTAGCTATTACCCCGTGAAGATCGGGGATCATTCACACGCTCT	357		
DB	70	CTGGAAATGGCCACCGTGGCGGTGTATCCCTACGAGGACCGCAATTCGGTGCACCGGTTG	129		
QY	358	TTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCACTCAAGGCGTACCTGGAC	417		
DB	130	AAGGCCGACGAGTCTCTACCAAGATCGGTGAGGAGGCCACCCCACTCCGCGCTACCTGTCC	189		
QY	418	ATCGATGAAATTATCGGTGCAGCTTAAAGTAAAGCAGATGCCATTTACCCGGGATAC	477		
DB	190	GTCGACGAGATCGTCGGCACGCGCTGGCCCTCGCGCGGATCGATCTACCCCGGCTAC	249		
QY	478	GGCTTCCTGTCTGAAATGCCACGCTTGCCCGGAGTGTCCGGAACCGGCATTACTTTT	537		
DB	250	GGCTTCCTGTGCGAGAACCCCGATCTGGCGGCGGCTGCGCGGCGGCGGCATCACGTTT	309		
QY	538	ATTGGCCCCAACCCAGAGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAAACCGCC	597		
DB	310	GTCGCCCCCAGCGCCGAGGTGTCGAGCTCACCGGCGACAAGTCGCGGGCCATCGCGGCG	369		
QY	598	GCGAAGAAGGCTGCTGCCAGTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAG	657		
DB	370	GCGCGGCGCGGGTCTTCCGGTCTGGCCCTCTCGCCCGCGCTCGACCTCGGTGCAGGAG	429		
QY	658	ATCGTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGCAGATTGCCGTGGT	717		
DB	430	TTGCTGAGCGCCGCCGAGACGATGACGTTCCCGTGTTCGTCAGGCGGTTCGCCGCGGC	489		
QY	718	GGCGGACGCGGTATCGGTTTTGTGCTTCACTGATGAGCTTCGCAAAATTAGCAACAGAA	777		
DB	490	GGCGGCGCGGGGATCGCCGGGTCAACCGATCCGGGGCGCTGGCCGAGCGCATCGAGGCG	549		
QY	778	GCATCTCGTGAAGCTGAAGCGGCTTTCGGCGCATGGCGCGGTATATGTGCAACGTCTGTG	837		
DB	550	GCCAGCCGTGAGGCCGAGTCCGCGTTTCGGGACGCCCTCGGTGTTTCTCGAGCAGGCGGTG	609		

QY 1918 TCCGTGGAGGCTGGGGCGGCGGACCTACGATGTGGCGATGCGTTTCTCTTTGAGGAT 1977
Db 1690 TCGGTGAGTGTGGGGCGGAGCGGACTTACGCTGTGGCGCTGCGGTTTCTCAAGGAGGAC 1749
QY 1978 CCGTGGGACAGGCTCGACGAGCTCGCGAGGCGGATGCGGATGTAAACATTTCAGATGCTG 2037
Db 1750 CCGTGGGAGCGGCTGACGGCGCTGCGGAGGCGGATGCCGAACATCTGCCTTCAGATGCTG 1809
QY 2038 CTTTCGGCGCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGGCTT 2097
Db 1810 CTGCGTGGGCGTAAACCGTGGGTACACGCCCTATCCGGAGACGGTCAAGACGCGCTTC 1869
QY 2098 GTTAAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCGGCATCTTCGACGCGCTTAAAGAC 2157
Db 1870 GTCGCGGAGGCGACCGGCTACCGGCTACGACATCTTCGGCATCTTCGACGCGTTGAACAAC 1929
QY 2158 GTCTCCAGATGGTCCAGCAATCGACGCGATCCTGGAGACCAACACCGCGGTAGCCGAG 2217
Db 1930 GTCGACTCGATGGCCCGGCCATCGACGCGGTCCGGAAACCGGAAGCGCCATAGCCGAA 1989
QY 2218 GTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCCCTGAT 2277
Db 1990 GTGGCGATGTCTACACCGGCGACCTGTCCGATCCGGCCGAAAAGCTTTACACGCTGGAC 2049
QY 2278 TACTACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATCTTGGCCATTAAAG 2337
Db 2050 TATTACCTGAAGTGGCCGACCAAGATCGTGAAGCGGCGCGACGCTGCTGGCGATCAAG 2109
QY 2338 GATATGGCTGTCTGCTTCGCCAGCTCGCGGTAAACCAAGCTGGTACCCGCACTGCGCGCT 2397
Db 2110 GACATGGCCGCGCTGTGCGCGCACCGCGCGCGCGACGCTGGTGTGCGCGCTGAAGTCG 2169
QY 2398 GAATTCGATCTGCCAGTGCACTGTCACACCCACGACACTGCGGGTGGCCAGCTGGCAACC 2457
Db 2170 CGGTTGCACTGCGGTCACGTCGACACCCCATGACACGCGCGGCGGACAGCTGGCGACC 2229
QY 2458 TACTTTGTCGAGCTCAAGCTGGTGCAGATCTGTTGACCGTGTCTCCGCAACCACTGTCT 2517
Db 2230 TACGTGGCGGCTGTGCGAGCGCGGCGCGGATGCGGTGCAAGCGCGCGCGCGCGCTCGCC 2289
QY 2518 GGCACCACTCCAGCCATCCCTGTCTGCCATTTGTTGCTGCAATTCGCGCACACCCGTCGC 2577
Db 2290 GGAACCAACGACCGCGGCACTATCGTGTGCTGCGCGCGCGCGCGCGCGCGCTCGCC 2349
QY 2578 GATACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCGGTAATGCGGAAGCAGTGCGC 2637
Db 2350 GACACCGGTTGTCCCTGCCGCGGTGTGCGATCTGGAGCCGTAATGGGAGGCGCTGCCA 2409
QY 2638 GGACTGTACTGTCGATTTGAGTCTGGAAACCCAGGCCCAACCGGTGCGGTCTACCGCCAC 2697
Db 2410 AAGGTATACGCTCCCTTCGAATCCGCTCTTCGGCGCGCGACCGGCGGCTGTATCAACCAC 2469
QY 2698 GAAATCCAGGCGGACAGTTGTCCAAACCTGCTGACAGGCCACCGCACTGGGCGCTTGGC 2757
Db 2470 GAGATCCCGGCGGCGCAATTGTGGAATCTGCTCAGCAGGCGATTGCGCTGGGACTCGGC 2529
QY 2758 GATCGTTTCGAATCATCGAAGACAACTACGACGCGGTTAAATGAGATGCTGGGACGCCCA 2817
Db 2530 GACCCTGTCGAGGACATCGAAAACGCCCTACGCGCGCGCGCGCGCGGATTTGGGACACCTG 2589
QY 2818 ACCAAGGTACCCCATCTCTCAAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGCG 2877
Db 2590 GTCAAGGTACACCCGTCCAGCAAGGTGTTGGGCGACCTGGCGCTGGCGCTGGTGGTGCG 2649
QY 2878 GGTGTGGATCCAGCAGACTTTGCTGCCGATCCAAAAAGTACGACATCCCGAGACTCTGTC 2937
Db 2650 GGTGTGGCGCGCAGGACTTCGCCGAAGACCCCTCCGCTACGACATCCCGGATTCGGTG 2709
QY 2938 ATCGGCTTCTGCGCGGAGCTTGGTAACCTTCAGGTGGTGGCCAGAGCCACTGCGC 2997
Db 2710 ATCGGCTTCTGCGCGGAGCTCGGTGACCCGCGGCGGCTGGCCGAGCCGTTGCGC 2769
QY 2998 ACCCGCGCACTGGAAGCGCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCTTGAGGAA 3057

Db 2770 ACCAAGGCTTACAGGGCCGGGGCCGGCCAAGCCGAGCAGCCGCTGACGGCCCGAGGAC 2829
QY 3058 GAGCAGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTCAACCGCCTG 3117
Db 2830 GAAGCGGCTTGGCGCGCCCGGGTG-----CGCGACGCGAGCAGCGCTGAACCGGCTG 2883
QY 3118 CTGTTCCGAAAGCCAAACCGAAGAGTTCTCTACGGCCTGGTCGAAGGCCCGCGACATTGATCCGC 3177
Db 2884 CTGTTCCCGGACCGAACCAAGAGCTCGAGGACACCGCGAGCAGTACGGTGACACCTCG 2943
QY 3178 GCGCTGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCCGCGAGACTTTGATCCGC 3237
Db 2944 GGGCTGAGCGCCAAACAGTTCTTCTACGGATTGCGGACGGGCGAGCAACACCGCGTCGAA 3003
QY 3238 CTGCCAGATGTGCGCACCCACCTGCTTGTTCGCTGGATGCGATCTCTGAGCCAGACGAT 3297
Db 3004 CT---CGAGCGCGCGTGAGTTGCTGATCGGCTGGAGGCCATCTCCGATCCCGACGAA 3060
QY 3298 AAGGTATGCGCAATGTTGTGGCCAAAGTCAACGGCCAGATCCGCCCAATGCGTGTGCT 3357
Db 3061 CGCGCATGCGCACCGTATGTGCAATTCTCAACGGGACGCTGCGGCGCGGTGGTGGTGCGC 3120
QY 3358 GACCGTCCGTTGAGTCTGTCAACCGAAACCGCAGAAAAGGAGATTCCTCCAACAAGGCG 3417
Db 3121 GACCGCAGCATCGCCATCGACGTGCCCGCGCCGAGAGGCGCACCGGCGCAACCCCGAC 3180
QY 3418 CATGTTGCTGCACCAATTGCTGTCACCGGATTCACCGTGAATGTTGCTGAAGGTGATGAGT 3477
Db 3181 CACATCGCTGCCCGCTTCGCCGGGTGTGACGGTTCGCCGCGAGGTTCGCCGCGGAGGTC 3240
QY 3478 AAGGTGAGATGCAATCGCAATCATCGAGGCTATGAAGATGGAAGCAACATCACTGCT 3537
Db 3241 GAGGCCGCGCAGACCATCGCGACGATCGAGGCGATGAAGATGGAAGCGCGGTCAACGAC 3300
QY 3538 TCTGTTGACCGCAAAATCGATCGGTTGTGTTCTCTGTCGAACGAAGGTGGAAGTGGC 3597
Db 3301 CCGAAGTCGGCAAGGTGGCGCAATCGCCGTGTCCGACCGGTCAGGTCAAGTCAGGGCGGC 3360
QY 3598 GACTTGATCGTCT 3611
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RESULT 8

US-10-282-122A-28626

; Sequence 28626, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

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; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28626
; LENGTH: 3384
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28626

Query Match      35.7%; Score 1294.4; DB 12; Length 3384;
Best Local Similarity 62.0%; Pred. No. 0;
Matches 2099; Conservative 0; Mismatches 1276; Indels 9; Gaps 3;

QY 238 AAGATCTTGTAGCAAAACCGCGGGAATCGCGTCCGTCTTCCGTGCGAGCACTCGAA 297
Db 10 AAGGTGCTCTCGCCAATCGCGGGAGATCGCGATCCGGGCTTTCGTGCCCTACGAA 69

QY 298 ACCGGTGCAGCACGGTAGCTATTATACCCCGGTGAAGATCGGGGATCATTTCCACCGTCT 357
Db 70 CTGGCGTCCGAACCGTGGCCGTTTATCCGTACGAGGACCGCAATTCGACGACCGTCTC 129

QY 358 TTTGCTTCTGAAGCTGTCCGCAATTTGTTACCGAAGGCTCACAGTCAAGCGTACCTGGAC 417
Db 130 AAGCGGACGAGCTTTACAGATCGCGGACATCGGTCAACCCGGTGATGATACCTGTG 189

QY 418 ATCGATGAATATATCGGTGCAGCTAATAAAGTTAAAGCAGATGCCATTTACCCGGGATAC 477
Db 190 GTCACGAGATCGTCCGACCGGCCGTCGGGCGGTGCCGACGCTATCTACCCCTGGCTAC 249

QY 478 GGCTTCTCTGTGAAATGCCAGCTTCCCGCGAGTGTGCGGAAACCGGCATTACTTTT 537
Db 250 GGGTTTCTATCGAGATCCGGATCTGGTGGGCAATGCGCGCGGGGGGATCAGCTTC 309

QY 538 ATTGGCCCCAACCCAGAGTTCTTGTATCTCACCGGTGATAAGTCTCGCGCGGTAAACGCC 597
Db 310 GTCGGTCCAGCGCCGAAGTCTTGTAGCTGGTGGGAATAAGTCTCGGCCATTCGCGCG 369

QY 598 GCGAAGAGGCTGGTCTGCCAGTTTGGCGGAATCCACCCCGAGCAAAACATCGATGAG 657
Db 370 GCGCGGAAGCGGCTTGCCCGTGTGATGTCTCGCGCGCCCTCGGTTCGACGAA 429

QY 658 ATCGTTAAAGCGCTGAAGCCAGACTTACCCCATCTTTGTGAAGGCGAGTTGCCGGTGGT 717
Db 430 CTGCTGTCCGTTCCGCGCGCATGCCGTTTCCGTTGTTCTGTCGAAGGCAAGTTGCCG 489

QY 718 GCGGACCGGTATGCGTTTGTGTTTCACTGATGAGCTTCGCAATAGCAACAGAA 777
Db 490 GGGGCGGGGTATGCGTGTGCGGCAATATCGCGCGCTTCGCGAGGCGATCGAAGCC 549

QY 778 GCATCTCGTGAAGTGAAGCGGCTTTCGCGCATGGCGGTATGATGTCGAACGTGCTGTG 837
Db 550 GCCAGCCGGGAAGCGAGTCCGCGTTCGCGGACCCGACCGTCTATCTCGAGCAGGCAAGT 609

QY 838 ATTAACCTCAGCATATTAAGTGCAGATTCCTTGGCGATCACACTGGAGAAAGTTGTACAC 897
Db 610 ATCAATCCACGCCACATCGAGGTGAGATTTGGGGGACCAACCTCGCGACGTGATCCAT 669

QY 898 CTTTATGAACGTGACTGCTCACTGCGCGTGTGTCACCAAAAAGTTGTGAAATTCGCCA 957
Db 670 CTCATGAGCGTGAAGTGTGACGCTGCGCATCAGAAGGTCATCGAGCTGGCGGCC 729
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QY 958 GCACAGCATTTGGATCCAGAACTCGGTGATCGCATTTTGGCGGATGAGTAAAGTTCTGC 1017
Db 730 GCGCCGACCTGGACGCGCGAGTTGCGTTACAAGATGTGCTCGATGCGTCCCTTCGCC 789

QY 1018 CGCTCCATTTGTTACAGGCGCGGGAACCGTGGAAATCTTGGTGCATGAAAGGCAAC 1077
Db 790 CGCCATATCGGTACAGCTGCGCGGACCGTTCGAGTTCTTGTGACGAGCGAGGAGAG 849

QY 1078 CACGTCTTCATCGAAATGAACCAAGTATCCAGTTGAGCACACCGTGAAGAAATC 1137
Db 850 TATGTCTTCATCGAGATGAATCCCGGGTTTCAAGTGGAGCACACGTTGACCGAGGAT 909

QY 1138 ACCGAGGTGACCTGGTGAAGGCGCAGATCGCTTGGCTGTGGTCAACCTTGAAGAA 1197
Db 910 ACCGACGTGACCTGGTCCGACGACGCTGCGCATTTGCCCGGGGAGACGCTCGAACA 969

QY 1198 TTGGGTCTGACCCCAAGATAAGATCAAGACCCACGTTGAGCACACCGTGAAGAAATC 1257
Db 970 TTGGGCTTGGCGAGGAGGACATCGCACCGCATGGCGCGCACTACAGTGGCGGATCAC 1029

QY 1258 ACGGAAGATCCAAACAAACGGCTTCCGCCCCAGATACCGGAATATCACCGCTACCGCTCA 1317
Db 1030 ACCGAGGATCCGCCAAACGGCTTCCGCCCGGACACGGGCGCGATCAGCGGTTGGCAAC 1089

QY 1318 CCAGGCGAGCTGGCGTTCGTCTTACGAGTGCAGCTCAGTCCGTGGCGGAAATCACCGCA 1377
Db 1090 GCGGCGGTGCGGTGTCCGCTTGAACGCGCAGCAACCACTGGGCGCAGAAATCAGCCCG 1149

QY 1378 CACTTTGACTCCATGCTGGTGAATAATGACCTGCCGTGTTCGCACTTTGAAACTGCTGT 1437
Db 1150 TACTTCGACTCCATGCTGGTCAAGCTGACCTGTCCGGGCGCGTACCTCCCTACCGCAGTG 1209

QY 1438 GCTCGTGCACAGCGCGCTGGTGGTGAAGTTCACCGTGTCTGGTGTGCAACCAACATTTGT 1497
Db 1210 AGCCGTGCGCGCGCGGCGATCGCGGAGTTCGGGATCCGCGGGGTATCGACGAATATTCG 1269

QY 1498 TTCTTGGCTGCGTGTGTCGGGGAAGAGGACTTCACTTCCAAAGCGCATCGCCACCGGATTC 1557
Db 1270 TTCTTGAAGCGGTCTTGGATGACCGCGACTTCCGAGCGGCGCGGTCAACACGTCTCCTTC 1329

QY 1558 ATTGCGGATCACCGCACCTCTTCAAGGCTCCACCTGTGTATGATGAGCAGGACGCAATC 1617
Db 1330 ATTGATGAGCGCGCGCAGCTGTGACCGCGCGCGCTCGCGCGACCGCGGACCAAGATC 1389

QY 1618 CTGGATTACTTGGCAGATGTACCGGTGAACAAAGCCTCATATGTTGCTGCCATCAAGGATTT 1677
Db 1390 CTTAACCTTCTGGCGGATGTACCGTCAACCAACCCGATATGGCTGCGTCCGTCAACGATC 1449

QY 1678 GCAGCTCTTATCGATAAGCTGCTTAACATCAAGGATCTGCCACTGCCACGCGTTCCCGT 1737
Db 1450 TACCCGACGACAAAGCTGCCCGATCTTGATCTGCGGCGCGCACCAACCGCGGTTCCAAG 1509

QY 1738 GACCGCTGAAGCAGCTTGGCGCCAGCGCGCTTGTCTGCTGATCTCCGTGAGCAGGACGCA 1797
Db 1510 CAGCGACTAGTCAAGTTGGGCGCGGAAGGATTTGCTGCTGGCTGCGGAGTCCGCGCGG 1569

QY 1798 CTGGCAGTTACTGATACCACTTCCGCGATGCACACAGTCTTGTGCTTGGACCCGAGTC 1857
Db 1570 GTCGGGTCACCGATACCACTTCCGCGATGCTCAACAGTCTGTACTGGTACCCGAGTA 1629

QY 1858 CGCTCATTCGCACTGAAGCCTTCCGCGAGGCGCTCGCAAGCTGACTCCTGAGCTTTTG 1917
Db 1630 CGCACCGAGCTGTGCGGGTGGCACCGTATCTCGCGCGGACCATGCGCGAGCTGTTG 1689

QY 1918 TCCGTGGAGGCTGGGCGCGGACCTACGATGTGGCGATGCGTTTCTCTTTGAGGAT 1977
Db 1690 TCCGTGGAGTGTGGGCGCGTTCGACTTACGATGTGGCGTGGCTTCTCAAGGAGGAT 1749

QY 1978 CCGTGGGACAGGCTCGAGGCTGCGCGAGGCGGATGCCGAATGTAAACATTCAGATGCTG 2037
Db 1750 CCTTGGGAACGCTGGCCACACTGCGTGCAGCAATGCCCAATATCTGCTTGCAGATGCTA 1809

QY 2038 CTTGCGGCGCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTTCTGCGCGCGGCTT 2097
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; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26500
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-282-122A-26500

Query Match 35.7%; Score 1292.2; DB 12; Length 3381;
Best Local Similarity 62.0%; Pred. No. 0;
Matches 2095; Conservative 0; Mismatches 1273; Indels 9; Gaps 3;

QY	238	AAGATCTTGGTAGCAAAACCGCGCGGAAATCGCGTCCGTCTTTCCGTGAGCACTCGAA	297
Db	10	AAGTGTCTGTCGCCAATCGCGGGGAGATCGGATCCGGGCCCTTTTCGTGCGCCTACGAA	69
QY	298	ACCGGTGCAGCCACGGTAGCTATTATACCCCGGTGAAGATCGGGATCAATCCACCGCTCT	357
Db	70	CTGGCGTCCGAACCGTGGCGGTTATCCGTACGAGACCGCAATTCGACACCGTCTC	129
QY	358	TTTGTCTTGAAGCTGTCCGCATGTGTACCGAAGGCTCACCAGTCAAGGCGTACCTGGAC	417
Db	130	AAGCGGACGAGTCTTACCAGATCGCGGACATCGGTCAACCGGTGCATGCATACCTGTGC	189
QY	418	ATCGATGAATATTATCGTGCAGCTAATAAAGTTAAAGCAGATGCCATTTACCGGGATAC	477
Db	190	GTGACGAGATCGTCGCGACGCCCGCTCGGGCGGTGCGGACGCTATCTACCTGGCTAC	249
QY	478	GGCTTCCTGTCTGAAATGCCAGCTTGCCCGGAGTGCAGGAAACCGGCATTACTTTT	537
Db	250	GGTTTCTATCGAGAAATCCGATCTGGCTGCGGATGCGCGCGGCGGCGCATCAGCTTC	309
QY	538	ATTGSCCAACCCAGAGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGTAACCGCC	597
Db	310	GTGCTCCAGCGCGAAGTGTGAGTGGCTGGGATAAGTCTCGCGCCATCGCGCG	369
QY	598	GCGAAGAGGCTGGTCTGCCAGTTTGGCGGAATCCACCCCGAGCAAAAACATCGATGAG	657
Db	370	GCCCCGAAGCCGGCTTGCCCGTGTGATGTCTCGGCGCGCTCGGCCTCGGTGACGAA	429
QY	658	ATCGTTAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTGCCGTTGT	717
Db	430	CTGCTGCTGGTTGCGGCGGCAATGCCGTTTCCGTTGTTCTCAAGGCAGTTGCCGTTGC	489
QY	718	GGCGACCGGATATCGGTTTTGTTGCTTACCTGATGAGTTCGCAATTTAGCAACAGAA	777
Db	490	GGGGCCCGGGTATCGTCTGTCGGCGATATCGCGGCGCTTCGGAGGCGGATCGAAGCC	549
QY	778	GCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGGATATGTGCAACGTTGCTGTG	837
Db	550	GCCAGCCGGGAAGCCGAGTCCGGCGTTTCGGGACCCGACCGGTCTATCTCGAGCAGCAGTG	609
QY	838	ATTAACTCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACAC	897
Db	610	ATCAATCCACGCCACATCGAGGTGCAGATTCTTGGCGGACAACTTCGGCGACGTTGATCCAT	669
QY	898	CTTTATGAACGTGACTGCTCACTGCAGCGTGTGTCACCAAAAGTTGTGCAATTTGGCCCA	957
Db	670	CTCTATGAGCGTGAATGATGTGCAAGCTCGCCATCAGAAGTTCATCGAGTGGCGCCC	729
QY	958	GCACAGCAATTTGGATCCAGAACTGCGGTGATCGCATTTGTGGGATGCAGTAAAGTTCTGC	1017
Db	730	GGCCCGCACTTGGACGCCAGTTTGGGTTACAAGATGTGCGTGCATGCGGTTCGCTTCGCC	789
QY	1018	CGCTCCATTGGTTACAGGGCGCGGGAACCGTGGAAATCTTGGTTCGATGAAAGGGCAAC	1077
Db	790	CGCCATATCGGTACAGCTGCGCGGCGCACCGTTCGAGTTCTCTGCTGGACGAGCGAGGGAG	849
QY	1078	CACGTCTTCATCGAAATGAACCCACGTTATCCAGGTTGAGCACACCGTGAAGAGTC	1137

Db	850	TATGTCTTCATCGAGATGAATCCGCGGTTTCAGTTGGAGCACACGGTGACCGGAGATT	909
QY	1138	ACCGAGGTGACCTTGGTGAAGCGCGAGATGCGTTGGTGTCTGGTGAACCTTGAAGGAA	1197
Db	910	ACCGACGTGACCTTGGTCCGCGAGCCAGCTGCGCATTCGCCCGGGAGACGCTCGAACAA	969
QY	1198	TTGGGTCTGACCCCAAGATAAGATCAAGACCCACCGTGCAGCAGTGCAGTGGCGCATCACC	1257
Db	970	TTGGGCTTGGCGGAGGAGACATCGCACCGCATGCGCCGACATACAGTGGCGGATCACC	1029
QY	1258	ACGGAAGATCCAAACACGGCTTCGCCCGCAGATACCGGAACATATCACCGGTACCGCTCA	1317
Db	1030	ACCGAGGATCCGGCCAAACGGCTTCGGCGCGGACACGGGCGGATCAGCGCGTTGCGCACC	1089
QY	1318	CCAGCGGAGCTGGCGTTTGTCTTTGACGGTGCAGCTCAGTCCGTGGCGGAATCACCGCA	1377
Db	1090	GCGGCGGTGCCGTGTCCGCTTGACCGGACGACCAACCTGGCGCAGAAATCAGCCCG	1149
QY	1378	CACTTTGACTCCATGCTGGTGAATAATGACCTGCGGTGTTCCGACTTTTGAAACTGCTGT	1437
Db	1150	TACTTCGACTCCATGCTGTCAAGCTGACCTGTCCGGGCGGTGACCTCCCTACCGCAGTG	1209
QY	1438	GCTCGTGCACAGCGCGGTGGTGGTTCACCGGTCTGGTGTTCGCAACCAACATTTGGT	1497
Db	1210	AGCGTGGCGCGCGCGGATCGCGGAGTTCGGGATCCGGGGTATCGACGAATATTCG	1269
QY	1498	TTCTTCCGTGCGTTGTCGGGAAGAGGACTTTCACCTTCCAAAGCGCATCGCCACCGGATTC	1557
Db	1270	TTCTTCAAGCGTCTTGGATGACCCCGACTTCCGAGCGGCGCGGTCAACCACTCTTC	1329
QY	1558	ATTGCCGATCACCCGCACTCTTCAGGCTCCACCTGCTGATGATGAGCAGGAGCGCATC	1617
Db	1330	ATTGATGAGCGCGCGAGTGTGACCGCGCGCTCGGCCGACCGCGGCGCAAGATC	1389
QY	1618	CTGGATTACTTGGCAGATGTCACCGTGAACAAGCTTCATGTTGCGTCCAAAGGATGTT	1677
Db	1390	CTTAACCTTCTGGCCGATGTACCGTCAACAACCCGATGCTGCGTCCGTCAACGATC	1449
QY	1678	GCAGTCTCTATCGATAAGTGCCTAACATCAAGGATCTGCCACTGCCACCGGTTCCCGT	1737
Db	1450	TACCGGACGACAAGCTGCCGATCTTGATCTGCGGCGCGCACCAACCGCGCGGTCCAAG	1509
QY	1738	GACCGCTGAAGCAGCTTGGCCAGCGCGGTTTGGTCTGTTGATCTCCGTGAGCAGGACGCA	1797
Db	1510	CAGCGACTAGTCAAGTTGGGCGCGAAGGATTTGCTGTTGGTGGGAGTCCGCCGCG	1569
QY	1798	CTGGCAGTTACTGATACCACTTCGCGGATGCACACCAAGTCTTGTGCGACCCGAGTC	1857
Db	1570	GTGCGGTACCGATACCAATTCGGGATGCTCACCAAGTCTGCTACTGGCTACCCGAGTA	1629
QY	1858	CGTCAATTCGCACTGAAGCTTGGCGCAGAGCGCGTGCAGAAAGCTGACTCCTGAGCTTTTG	1917
Db	1630	CGCACCGCGGACTGTCCGGGTGGCACCGTATCTCGCGCGACCATGCGCGAGCTGTG	1689
QY	1918	TCCGTGGAGGCTTGGGCGCGCGACCTACGATGTGGCGATGCGTTTCTCTTTGAGGAT	1977
Db	1690	TCCGTGGAGTGTGGGCGGTTGCGACTTACGATGTGGCGTGGCTTTCTCAAGGAGGAT	1749
QY	1978	CCGTGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATTCAGATGCTG	2037
Db	1750	CCCTGGGAACGGCTGGCCACACTGCGTGCAGCAATGCCCAATATCTGTTGCAGATGCTA	1809
QY	2038	CTTCGCGCGCGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCCGCGTTT	2097
Db	1810	TTGCGGGCGCGCAATACCGTGGGTACACCGCGTACCGCGGAATCGTGACGTCCGCGTTT	1869
QY	2098	GTTAAGGAAGCTGCCAGCTCCGGGTGGACATCTTCGCAATCTTCGACCGCTTAACGAC	2157
Db	1870	GTGCAAGGAAGCAACAGCCACCGGTATCGACATCTTTTCGTATCTTCGACGCGCTCAACAC	1929
QY	2158	GTCTCCAGATGCTCCAGCAATCGACGCGAGTCTCTGGAGACCAACACCGCGGTAGCCGAG	2217

Db 1930 ATCGAGTCGATCGCTCCGGCGATCGACCGCAGTACCGGAACAGGTTCTGCGATACGAGAA 1989
QY 2218 GTGGCTATGGTTATTCTGTGTGATCTCTCTGATCCAAATGAAAAAGCTCTACACCCCTGGAT 2277
Db 1990 GTCCGATGTCTACACGGGCGACCTTACCGATCCGGGTGAACAGCTGTACACGCTGGAC 2049
QY 2278 TACTACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGTCAACATCTTGGCCATTAA 2337
Db 2050 TACTACCTGAAGTGGCTGAGCAGATCGTGGACCGCGCGCCCTCAAGTTGGTCAAGGATCAAG 2109
QY 2338 GATATGGCTGTCTGTCTCGCCAGCTGGCGGTAAACAAAGCTGGTCAACCGCACTGGCCGT 2397
Db 2110 GATATGGCTGGAATGTTGCGCCCGCGCGCTCAAGTTGGTCAAGGATCAAGGATCAAG 2169
QY 2398 GAATTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACC 2457
Db 2170 CGCTTCGACCTGCCCGCTTACCTGCACACCCACGACACACCGGGTGGCCAGCTGCCACG 2229
QY 2458 TACTTTGCTGAGCTCAAGCTGGTGCAGATGCTGTGACCGGTGTTCCGCAACCACTGTCT 2517
Db 2230 TATGTGGCCGCTTGGACACCGCGGCGCGATGCTGACCGCGCGCGCGCGCTGGCG 2289
QY 2518 GGCACCACTCCAGCCATCCCTGCTGCTGCAATGTTGCTGCAATCGCGCACACCCGCTGCG 2577
Db 2290 GGAACGACCAAGCCAGCCCGCGCTGAGCTCGATCGTTGCTGCGCGCTGCCACACCGAGTAC 2349
QY 2578 GATACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGCGC 2637
Db 2350 GACACCGGCTGTGCTTTTCGGCGGTGTGCGCCCTGGAGCCGTACTGGGAGCGTTACGA 2409
QY 2638 GGACTGTACCTGCCATTTGAGTCTGGAACCCAGGCCCAACCGGTGCGCTCTACCGCCAC 2697
Db 2410 AAAGTGTATGCGCCGTTGAGTCTGAGTCTGGGTTGCGGGGCGCGACCGGGCGGGTTTATCACCC 2469
QY 2698 GAAATCCAGCGGACAGTGTCCAACTGCGTGCACAGGCCACCGCACTGGGCTTGGC 2757
Db 2470 GAGATTCGGGCGGCAACTGTCTAATCTGCGGCAGCAAGCAATTGCTCTTGGTCTGGGA 2529
QY 2758 GATCGTTTCGAACCTCATCGAAGACAACTACGACGCCGTTAATGAGATGCTGGGACGCCCA 2817
Db 2530 GATCGATTGGAAGAGATCGAAGAGGCCCTACCGGGGCGCGACCGAGTGTGGCAGGCTG 2589
QY 2818 ACCAAGGTCAACCCATCTCTCAAGGTTGTTGGGACCTCGCACTCCACTCGTTGGTGGC 2877
Db 2590 GTTAAGGTCAACGCCAACGTCCAAAGTGTGCGCGATCTGGCGTGGCACTGGTGGCGCC 2649
QY 2878 GGTGTGGATCCAGCAGACTTGTGCTGCCGATCCCAAAAGTACGACATCCAGACTCTGTC 2937
Db 2650 GGTGTGAGTGCAGACGAATTGCTCCGATCCAGCGGATTTGGCATCCCGGAATCGGTA 2709
QY 2938 ATCGGTTCTGCGGCGGAGCTTGGTAACCCCTCCAGGTGGCTGGCCAGAGCCACTGCGC 2997
Db 2710 CTGGATTTCTGCGGGCGAGTGGGTGATCCGCGCGCGGTGGCCGCAACCGCTGCGC 2769
QY 2998 ACCCGGCACTGGAAGCGCGCTCCGAAGGCAAGGCAACCTCTGACGGAAGTTCTGTAGGAA 3057
Db 2770 ACTGGGCGCTGGCCGCTGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2826
QY 3058 GAGCAGGCGCACCTCGACGCTGATGATTCCAAAGGAACGTGCAATAGCCTCAACCGCCTG 3117
Db 2827 GACGAGATTGCCCTATCGTCTGCTCGAGCCAAAG---CGTCAGGCCACCCCTGAACAGGCTG 2883
QY 3118 CTGTTCCGGAAGCCAAACCGAAGATTCTCTGAGCACCGTCCGCGCTTCGGCAACACCTCT 3177
Db 2884 TTATTTCCAGTCCAAACAAAGGAATTCAATGAGCACCGGAAGCCCTACGCGGACACGTCG 2943
QY 3178 GCGCTGATGATCGTGAATTTCTTACGGCCCTGGTTCGAAGCCCGCGAGACTTTGATCCGC 3237
Db 2944 CAATTGCGGCCAACCAAGTTCTTCTATGTTCTGCGCCCAAGGTGAAGAGCATCGGTTAAG 3003
QY 3238 CTGCCAGATGTGCGCACCCCACTGCTTGTTCGCTGGATGCGATCTCTGAGCCAGACGAT 3297
Db 3004 CTG---GAGCGTGGGTGGAGCTGTTGATCGGGCTGGAGGCCATTTCGGAACCCGACGAA 3060

QY 3298 AAGGTATGCGCAATGTTGTGGCCAAACGTCAACGGCCAGATCCGCCCAATGCGTGTGCGT 3357
Db 3061 CGCGCATGCGAAACGGTGTGATGTCATCTCAACGGGCGAGCTGCGGCGGTGCTAGTGGC 3120
QY 3358 GACCGTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGAGATTCCTCCAACAGGGC 3417
Db 3121 GACCGCAGCATGCGAGTCCAGTCCGTTCCGGCCCGAGAAAGCCGACCGCGGCAATCCCGGA 3180
QY 3418 CATGTTGCTGCACCATTCGTTGCTGTGTGTACCGTGTGCTGAAAGGTGATGAGGTC 3477
Db 3181 CACATCGCCGCGCCATTGCGCGAGTCTGTCACGGTCCGGGTGTGCGTCCGGGAGCGGGTC 3240
QY 3478 AAGGTGAGATGAGTGCATCGCAATCATCGAGGCTATGAAGATGGAAGCAACATCACTGCT 3537
Db 3241 GGCGCCGCGCAACCATCGCCACCATCGAGGCGATGAAGATGGAAGCCCGATCACCGCC 3300
QY 3538 TCTGTTGACGGCAAAATCGATCGGTTGTGTTGTTCTGCTGCAACGAAGGTGGAAGGTGGC 3597
Db 3301 CCGGTTGCGGACCGTGGAGCGGGTGGCGGTGTCCGACACCGCCAGGTGGAGGGCGGA 3360
QY 3598 GACTTGATCGTCTGCT 3614
Db 3361 GACCTGTTGTTGTTGTT 3377

RESULT 10
US-09-917-800A-1566
; Sequence 1566, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1566
; LENGTH: 3945
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012744
US-09-917-800A-1566

Query Match 18.8%; Score 681; DB 9; Length 3945;
Best Local Similarity 54.2%; Pred. No. 3.2e-197;
Matches 1521; Conservative 0; Mismatches 1260; Indels 24; Gaps 6;

QY 233 TCAAAAGATCTTGGTAGCAACCCGCGCGAAATCGCGTCCGTGCTTTCCGTGCAGCAC 292
Db 144 TCAAGAAAGTAATGGTGGCCAAACAGAGGTGAGATTGCCATCCGAGTGTTCGTGCTGCA 203
QY 293 TCGAAACCGGTGCAGCCACCGTAGCTATTTACCCCGTGAAGATCGGGATCAATCCACC 352
Db 204 CAGAGCTGGGTATCCGCACAGTGGCTGTCTACTCGGAGCAGGACACAGGCCAGATGCACC 263
QY 353 GCTCTTTTGTCTCTGAAGCTGTCCGATTTGGTA CCGAAGGCTCACAGTCAAGGCTTACC 412
Db 264 GGCAGAAAGCTGATGAAGCCTACCTTANTGGCCGTGGCTGGCTCCTGTGCAAGCCTACC 323
QY 413 TGGACATCGATGAAATTA TCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTACCCGG 472
Db 324 TGCACATTCAGACATCAATTAAGGTGGCCAAAGGAGAAATGGTGTAGATGCTGTGCACCCCTG 383
QY 473 GATACGGTTCCTGTCTGAAATATGCCAGCTTGGCCCGAGTGTGCGGAAACCGGATTA 532
Db 384 GCTATGGGTTCCTCTCAGAGAGAGCAGACTTTGCCAGGCCTGCCAAGATGCTGGAGTCC 443
QY 533 CTTTATTGGGCCAAACCCAGAGGTTCTTGATCTCA CCGGTGATAAGTCTCGCGCGTAA 592
Db 444 GATTCAATGGTCCAAAGCCAGAGGTGGTCCGCAAGATGGGAGACAAGGTGGAAGCCCGGG 503
QY 593 CCGCCGGAAGAAGGCTGGTCTGCCAGTTTGGCGGAATCCA --- CCGGAGCAAAACA 649
Db 504 CCAATTGCCATTGCTGCAGGCGTTCCAGTGGTCCCTGGCACTAATTC CCCCATCAATCCC 563
QY 650 TCGATGAGATCGTTAAAGCGCTGAAGCGCTTGAAGCCAGACTTACCCCACTTTGTGAAGGCAGTTG 709
Db 564 TGCATGAGGCACACAGATTCTCTAACACCTATGGTTTCCCTAATATCTTCAAGGCTGCT 623
QY 710 CCGGTGGTGGCGAGCGGATATGCGTTTGTGCTTTCACCTGATGAGCTTCGCAATTAG 769
Db 624 ATGAGGTGGGCGCGTGGCATGAGGGTTGTGCATAGCTACGAGGAGCTGGAAGAGAATT 683
QY 770 CAACAGAAAGCATCTCGTGAAGCTGAAGCGCTTTCGGCGATGGCGGATATATGTCCAAC 829
Db 684 ACACCGGCGCTACCTTGAGGCTTGGCAGCCTTTGGGAATGGGCACTGTTTGTGGACA 743
QY 830 GTGCTGTGATTAAACCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAG 889
Db 744 AATTCAATTGAGAAGCCAAGACACATTGAGGTGCAGATCCTAGGGACCAATATGGGAACA 803
QY 890 TTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCTGTCAACCAAAAAGTTGTGCAAA 949
Db 804 TCTTGCACTTTGATAGCGGGACTGCTCCATCCAGCGCGGCACAGAGGTGGTAGAGA 863
QY 950 TTGCGCCAGCAGCAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAA 1009
Db 864 TTGCCCCCTGTACCCACCTGGACCCCACTTCGGTCAACGCCCTCACCAGTGACTCTGTCA 923
QY 1010 AGTTCTGCGCTCCATTGGTTACCAGGCGCGGGAACCGTGGAAATTTCTTGGTCGATGAAA 1069
Db 924 AACTTGCCAAAGCAGGTGGCTATGAGAATGCAGGCACTGTGGAGTTCCTGGTGGACAAGC 983
QY 1070 AGGGCAACCCAGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACTG 1129
Db 984 ATGGCAAGCACTACTTTCATCGAGGTCAATTC CCGCTGCAGATCCATGTGTCCGAAGGCCGAGCC 1043
QY 1130 AAGAAGTCA CCGAGGTGGAACCTGGTGAAGCGCGAGATGCGCTTGGCTGCTGGTGCAACCT 1189
Db 1044 AGGAGATTACAGATGTGGACCTGGTCCATGCTCAGATCCATGTGTCCGAAGGCCGAGCC 1103
QY 1190 TGAAGGAATTGGGTCTGACCCCAAGATAAGATCAAGACCCACCGTGCAGCACTGCAGTGCC 1249
Db 1104 TGCCTGACCTAGGCTGCGGCAGGAAACATCCGAATCAATGGTGTGTGCCATTTCAGTGTC 1163
QY 1250 GCATCACCA CCGAAGATCCAAACAACGGCTTCGCGCCAGATACCGGAACCTATCACCGCGT 1309
Db 1164 GGGTCACCACTGAGACCCCTGCACGCACTTCCAGCCAGACACTGGCCGCAATTGAGGTTT 1223
QY 1310 ACCGCTCACAGGCGGAGCTGGCGTTTCGTCTTGACGGTG --- CAGCTCAGCTCGGTGGCG 1366

Db 1224 TCCGGAGTGGTGAGGGCATGGGSCATCCGCCTGGACAATGSCCTCAGCATTC CAGGGAGCTG 1283
QY 1367 AAATCACCGCACACTTTTGACTTCATGCTGGTGAATAATGACCTGCCGTGGTTCCGACTTTG 1426
Db 1284 TCATATCCCCCACTATGACTCCCTGCTCGTCAAAGTCAATGCCCATGGCAAAAGACCACC 1343
QY 1427 AAACGTGCTGTGCTCGTGCACAGCGCGCTTGGCTGAGTTCACCGTGTCTGGTGTGCAA 1486
Db 1344 CTACAGCTGCCACCAAGATGAGCAGAGCCCTGGCGGAGTTCGCTGTCCGAGGTGTAAGA 1403
QY 1487 CCAACATTTGGTTTCTTGGTGGCTTGTGCGGGAAGAGGACTTCACTTCCAAGCGCATCG 1546
Db 1404 CCAACATCCCCTTCTGTCAGAAATGTCTCAACAAC CAGCAGTTCCTAGCGGCAATTGTGG 1463
QY 1547 CCACCGGATTCATTTGCCGATCACCGGCACCTCCTTTCAGGCTCCACCTGCTGATGATGAGC 1606
Db 1464 ACACCCAGTTCATCGATGAGAACCCCGAGCTGTTCCAGCTGGCGCCTGCACAGAACCCGG 1523
QY 1607 AGGACCGCATCCTGGATTACTTGGCAGATGTCA CCGGTGAACAAGCCTCATGGTGTGCGTC 1666
Db 1524 CCCAGAAGTGTACATTACCTTGGACAGCTCATG TGTCAATGGCCCTACCACCTCCAATCC 1583
QY 1667 CAAAGGATGTGCAGCTCCATATCGATAAGC --- TGCCTAACATCAAGGATCTGCCAC 1720
Db 1584 CCGTCAAGGTCACTCCAGCCCTGTGACCCCATTTGTTCTCTGTTGGTGCCATAGGCCAC 1643
QY 1721 TGCCACGCGCTTCCCGTGACCCGCTGAAGCAGCTTGGCCAGCGCGTTCGTGCTGATC 1780
Db 1644 CCCCAGCTGGTTTCAGAGACATCCTTCTCGAGAGGGGCCAGAGGCTTTGCCAGAGCTG 1703
QY 1781 TCCGTGAGCAGGACGCACTGGCAGTTACTGATACCA CCTTCCGCGATGCACACCAAGTCTT 1840
Db 1704 TGCGGAATCACAGGGGCTGCTGCTAATGGA CACAACCTTCCGGGATGCCACCAAGTCAC 1763
QY 1841 TGCTTGGCACCCGAGTCCGCTCATTTCCGACTGAAG CCTGCGGCGAGAGGCCGTGCGAAAGC 1900
Db 1764 TACTTGGCACTAGAGTGGGCACACACAGCATCT CAAAAGATTGCACTTACCTTACCTTGC 1823
QY 1901 TGACTCCTGAGCTTTTGTCCGTGGAGCCCTGGGCG CGGCACTTACGATGTGGCGATGC 1960
Db 1824 ACTTCAACAACCTCTTCAGCATAGAGAACTGGG GAGGAGCCACATTTGACGTGGCCATGC 1883
QY 1961 GTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGA CAGCTGCGGAGGCGATGCCGAATG 2020
Db 1884 GCTTCTTGTATGAGTGCCTTGGCGCGGCTCCAG GAGCTCCGGAGCTCATCCCCAACA 1943
QY 2021 TAAACATTCAGATGCTGCTTCCGCGCCGCAACAC CCGTGGGATACACCCGTACCCAGACT 2080
Db 1944 TCCCATTCAGATGCTACTGAGGGGGCCAAATGT GTGGGCTACACCAACTACCCCTGACA 2003
QY 2081 CCGTCTGCGCGGCTTGTTAAGGAAGTGCAGCTCC GCGGTGGACATCTTCCGCTATCT 2140
Db 2004 ACGTGGTCTTCAAGTTCGTGAGGTGGCCAAAGAG AATGGCATGGAGCTTCCGGATCT 2063
QY 2141 TCGACGCGCTTAACGACGCTCTCCAGATGCGTCCAG CAATCGACGAGTCTCTGGAGACCA 2200
Db 2064 TTGACTCCCTTAACCTACCTGCCAAACATGCTGT GGGCATGGAGCAG --- CTGGCAGTG 2120
QY 2201 ACACCGGCTAGCCGAGGTGGCTATGGCTTATTTCT GGTGATCTCTCTGATCCAAATGAAA 2260
Db 2121 CTGGGGGTGTGGTGGAAAGCTGCCATCTCCTACA CCGGTGACGTGGTGAACCCAGTCGCA 2180
QY 2261 AGCTCTACACCTCGGATTAATAAGATGGCAGAGGAG ATCGTCAAGTCTGGCGCTC 2320
Db 2181 CTAAATACTCACTGGAGTACTACATGGGCTTAGCT GAAGAACTGGTGGAGCCGGCACTC 2240
QY 2321 ACATCTTGGCCATTAAGGATATGGTGGTCTGCTTGC CCCCAGCTGCGGTAACCAAGCTGG 2380
Db 2241 ACATCCTCTGCATTAAGGACATGGCAGGCTGTGA AGCCTGCAGCATGCACCATGCTGG 2300
QY 2381 TCACCGCACTGG --- CCGTGAATTCCGATCTGCCAG TGCAGCTGCACACCCACGACACTG 2437

Db 2301 TCAGCTCCCTCCGGACCGGTTCCCGACCTCCCACTGCACATCCATACCCATGACACAT 2360
QY 2438 CGGGTGGCCAGCTGGCAACCTACTTTTGTCTGAGCTCAAGCTGGTGCAGATGCTGTTGACG 2497
Db 2361 CAGGGTCAGGTGTGGCAGCCCATGTTGGCCTGTGCACAAGCTGGGCTGATGTTGTGGATG 2420
QY 2498 GTGCTTCCGCACCACTGTCTGGCACCACCTCCAGCCCATCCCTGTCTGCCATGTTGTGCTG 2557
Db 2421 TGGCAGTCGACTATGTTCTGGGATGACCTCACAGCCACAGCATGGGGGCCCTGGTGGCCT 2480
QY 2558 CATTCCGCGCACACCCGTCCGATACCCGTTTGAAGCTCGAGGCTGTTTCTGACCTCGAGC 2617
Db 2481 GTACCAAAGGGACTCCTCTGGACACAGAGGTACCCCTGGAGCGTGTGTTGACTACAGTG 2540
QY 2618 CGTACTGGGAAGCAGTGGCGGACTGTACCTGCCATTGA-----GTCTGGAACCCCGAG 2671
Db 2541 AGTATTGGGAAGGGCTCGGGGCTGTATGACAGCCTTTGATTGACCGGCTACCATGAAGT 2600
QY 2672 GCCCAACCGGTGCGGTCTACCGCCACGAAATCCAGGCGGACAGTGTCTCAAACCTGCGTG 2731
Db 2601 CTGGCAACTCAGACGTGTATGAGAAATGAGGATCCAGGGGCCAGTACACCAACCTACT 2660
QY 2732 CACAGGCCACCGCACTGGGCTTTCGGGATCGTTTCGAACTCATCGAAGACAACTACGCGAG 2791
Db 2661 TCCAGGCCACACAGCATGGGACTTGGCTCCAAGTCAAGGAGGTCAAGAAGGCCTATGTGG 2720
QY 2792 CCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCAACCCATCCTCCAAGGTTGTTGGCG 2851
Db 2721 AGGCTAACCAAGATGCTGGGGACCTCATCAAGGTGACACCATCCTCCAAGATTGTGGGG 2780
QY 2852 ACCTCGCACTCCACCTCGTTGGTGGGATCCAGCAGACTTTGCTGCCGATCCAC 2911
Db 2781 ATCTGGCCAGTTTCATGGTGAGAACCGGTTGAGCCGGGCGAGGCGCAAGCTCAGGCGAG 2840
QY 2912 AAAAGTACGACATCCAGACTCTGTATCGGTTCTCGCGGCGGAGCTTGGTAACCTC 2971
Db 2841 AAGAGCTGTCTTCCCGCTCTGTGTGGAGTCTCTGAGGCTTACATTGGCATTCCCC 2900
QY 2972 CAGGTGGCTGGCCAGAGCCACTGCGCACCCCGGCACTGGAAGGCC 3016
Db 2901 ATGGGGTTTCCCTGAACCCCTCCGTTCTTAAGGTGCTAAAGGACC 2945

RESULT 11

US-09-880-107-3029
; Sequence 3029, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3029
; LENGTH: 4017
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 S72370
US-09-880-107-3029

Query Match 18.7%; Score 677.4; DB 9; Length 4017;
Best Local Similarity 54.4%; Pred. No. 4.1e-196;
Matches 1525; Conservative 0; Mismatches 1256; Indels 24; Gaps 7;

QY 233 TCAAAAAGATCTTGGTAGCAAAACCGCGCGAAATCGCGTCCGTGCTTCCGTGCAGCAC 292
Db 192 TCAAGAAAGTCATGGTGGCCAAACAGAGGTGAGATTGCCATCCGTGTGTTCCGGGCTGCA 251
QY 293 TCGAAACCGGTGCAGCCACGGTAGCTATTACCCCGGTGAAGATCGGGGATCATTCACC 352
Db 252 CGGAGCTGGCATCCGACCGTAGCCATCTACTGTAGCAGGACACGGGCCAGATGCACC 311
QY 353 GCTCTTTTGTCTTGAAGCTGTCCGCATTTGTACCGAAGGCTACCAAGTCAAGGCGTACC 412
Db 312 GGCAGAAAGCAGATGAAGCCTATCTCATCGGCGCGGCTGGCCCCGTGCAGGCTACC 371
QY 413 TGGACATCGATGAAATATCGGTGCAGCTAAAAAAGTTAAAGCAGATGCCATTTACCCGG 472
Db 372 TGCACATCCCAAGACATCATCAAGGTGGCCAAAGGAGAACAAACGTAGATGCAGTGCACCTG 431
QY 473 GATACGGCTTCTGTCTGAAATGCCCCAGCTTCCCGGAGTGTCCGGAACAAACGGCATTA 532
Db 432 GCTACGGGTTCTCTGTAGCGAGCGGACTTCGCCAGGCTGCCAGGATGCAGGGGTCC 491
QY 533 CTTTATTGGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCGGTAA 592
Db 492 GGTATTGTCCAAAGCCAGAAAGTGGTCCGCAAGATGGGAGACAAGGTGGAGGCCCGG 551
QY 593 CCGCCGGAAGAGGCTGGTCTGCCAGTTTGGCGG--AATCCACCCCGAGCAAAACA 649
Db 552 CCATCGCCATTGCTGCGGGTGTCCCGTGTCTCCCTGGCACAGATGCCCCCATCAGTCCC 611
QY 650 TCGATGAGATCGTTAAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTTG 709
Db 612 TGCATGAGGCCACGAGTTCTCCAACACCTACGGCTTCCCATCATCTTCAAGGCGGCT 671
QY 710 CCGGTGGTGGCGGACGCGTATCGCTTTTGTGTTTGTCTTCACTGATGAGCTTCGCAATTAG 769
Db 672 ATGGGGTGGGGGCGTGGCATGAGGGTGTGCACAGCTACGAGGAGCTGGAGGAGATT 731
QY 770 CAACAGAAGCATCTCGTGAAGCTGAAGCGGTTTCGGCGATGGCGGCTATATGTCGAAC 829
Db 732 ACACCCGGCCTACTCAGAGGCTTGGGAAATGGGCGCTTGTGTGGAGA 791
QY 830 GTGCTGTGATTAAACCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAG 889
Db 792 AGTTTCATCGAGAGCCACGGCACATCGAGGTGCAGATCTTGGGGACAGTATGGGAACA 851
QY 890 TTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGCTCGTCACCAAAAAAGTTGCGAAA 949
Db 852 TCCTGCACCTGTACGAGCGAGACTGCTCCATCCAGCGCGGCACCAAGAAGTGTGTCGAGA 911
QY 950 TTGCGCCAGCACAGCATTTGGATCCAGAACTCGCTGATCGCATTTTGTGCGGATGCAGTAA 1009
Db 912 TTGCCCCCGCGCCACCTGGACCCCGAGCTTCGGACTCGGCTCACACCGACTCTGTGA 971
QY 1010 AGTTCTGCCGCTCCATTGGTTACCAGGGCGGGGAACCGTGGAAATTTCTTGGTCGATGAAA 1069
Db 972 AACTCGCTAAACAGGTGGGCTACGAGAACCGAGGCACCGTGGAGTTCTTGGTGGACAGGC 1031
QY 1070 AGGGCAACCAAGCTTTCATCGAAATGAACCCAGTATCCAGGTTGAGCACACCGTGACTG 1129
Db 1032 ACGGCAAGCACTACTTCATCGAGGTCAACTCCCGCTGCAGGTGGAGCACACCGTCCACAG 1091
QY 1130 AAGAAAGTCACCGAGGTGGACCTGTGAAGGCGCGAGATGCGCTTGGCTGTGTCGAACCT 1189
Db 1092 AGGAGATCACCGACCGTAGACCTGGTCCATGCTCAGATCCACGTTGGCTGAAGGACGAGGCC 1151
QY 1190 TGAAGGAATTGGGTCTGACCCCAAGATAAGATAAGAACCCACCGTGCAGCTGCAGTGCC 1249
Db 1152 TACCCGACCTGGGGCTGCGGACGAGGAGAACATCCGCATCAACGGGTGTGCCATCCAGTGCC 1211
QY 1250 GCATCACCAACGGAAGATCCAAACAAACCGGCTTCCGCCCCAGATACCGGAATCATCACCGCGT 1309
Db 1212 GGTTCACCAACCGAGGACCCCGCGCCACCGTTCCAGCCGGACACCGGCCGCAATTGAGGTGT 1271

Db	1	AAGATCCTCATCGCCAACCGTGGTGAGATCGCCATCCGGGTGATCGGGCGGCAACGAG	60
QY	298	ACCGGTGACGACCGTAGCTATTTACCCCGGTGAAGATCGGGGATCATTTCCACCGCTCT	357
Db	61	ATGGGCAAGAAACCGTGCCTCTATGCGGAGGAAGACAAGCTCTCGCTCCACCGCTTC	120
QY	358	TTTGTCTTGAAGCTGTCCGCAATTGGTACCGAAGGCTCACCAAGTCAAGGCGTACCTGGAC	417
Db	121	AAGCGGACGAGGCTTACCGGATCGGCGAGGCTCTCGCCCGTGGGCGCTATCTCTCG	180
QY	418	ATCGATGAATATCGGTGCAGCTTAAAGTTAAAGCAGATGCCATTTACCCGGGATAC	477
Db	181	ATCCCGGAGATCATCCGCTGGCGCAGATGTGGGCGCCGATGCGATCCACCCGGGCTAC	240
QY	478	GGCTTCCGTCTGAAAAATGCCAGCTTCCCGCGAGTGTGCGGAAAAACGGCATTACTTTT	537
Db	241	GGCTTCTGTGAGAAACCCCGATTTCTGTGAGGCTTGCAGCGCAGCGGCGCATCGCTTC	300
QY	538	ATTGGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGGCGGTAAACCGCC	597
Db	301	ATCGGCCGGAAGGCGGAGACGATCGCGCGCTCGGCGACAAGGCTTCGGGCCCGCGCGTG	360
QY	598	GCGAAGAAGGCTGTCTGCCAGTTTGGCGGAATCC--ACCCCGAGCAAAAAACATCGAT	654
Db	361	GCCATGGCCGCGGCGTCCCGGTGATCCCGGCGACCGAGGTGTGGCGCAGCATATGGAG	420
QY	655	GAGATCGTTAAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGCAGTTGCCGGT	714
Db	421	GAGATCAAGCGGCGGCGCGAGATCGGCTATCCGCTGATGCTCAAGGCTCGTGGGCG	480
QY	715	GGTGGCGGACCGCGTATCGCTTTTGTGCTTCACTGTATGAGCTTCGCAAAATTAGCAACA	774
Db	481	GGCGGTGGCGGCGCATCGGCCCATCACTTCCGAGCGCGAGCTGGCGGACAAGGTGCGC	540
QY	775	GAAGCATCTCGTGAAGCTGAAGCGGCTTTCGSCGATGGCGGCTATATGTCGAACGTGCT	834
Db	541	GAGGGCCGACGCGAGGCGAGGCGGCTTCGCAACGCGGAGGGCTATCTCGAGAAGATG	600
QY	835	GTGATTAAACCTCAGCATATTGAAGTCAGATCCTTGGCGATCACACTGAGAAAGTTGTA	894
Db	601	ATCCAGCGCGCGCCACGTCGAGGTGCAGATCTCGGCGACAATAACGCGCGATCTAC	660
QY	895	CACCTTTATGAACGTGACTGCTCACTGCAGCGTCTGCACCAAAAAGTTGTCGAAATTGCG	954
Db	661	CATCTCTACGAGCGGACTGCACCGTGCAGCGGCGCAACCAAGAAGTCTGAGCGCGCG	720
QY	955	CCAGCACAGCATTTGGATCCAGAACTCGGTGATCGCATTTGTGCGGATGAGTAAAGTTC	1014
Db	721	CCCGCGCTTATCTCACCGAGGACGCGGACAGAGATCTCGAGCTCGGCGCGCGGATC	780
QY	1015	TGCCGCTCCATTGGTTACAGGGCGCGGGAACCGTGGAAATCTTGGTCGAT--GAAAAG	1071
Db	781	TGCGCCCATGTGAATTACGAATGCGCGGCGACGGTTCGAGTTCTGTATGGATATGGAATCG	840
QY	1072	GGCAACCACGCTTTCATCGAAATGAACCCACGTCATCCAGGTTGAGCACACCGTGACTGAA	1131
Db	841	GAGAAATTCTATTTCATCGAGGTCAATCCGCGGGTTCAGGTTCGAACATACCGTCAACCGAG	900
QY	1132	GAAGTCACCGAGGTGGAACCTGGTGAAGGCGCAGATGGCTTGGCTGTGGTGCACACCTTG	1191
Db	901	GAAGTGACGGGCATCGACATCGTGCAATCCCAGATCCGATCGCGGAAGGGCGACGCTG	960
QY	1192	AAGGAATTGG-----GTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGACTGCAG	1245
Db	961	GCCGAGGCAACCGGATGCGCGAGCCAGGACGACATCAAGCTCTCGGGCCATGGCTGCAG	1020
QY	1246	TGCCGCTACCCACGGAAGATCCAAACACGCGCTTCGCGCCAGATACCGGAACCTATCACC	1305
Db	1021	TGCCGCGTCAACGACCGAGATCCGCAGAACAAATTTCAATCCGACTACGGCCGCTCACC	1080
QY	1306	GCGTACCGCTCACGAGCGGAGCTGGCGTTCTGTCTTGACGGTG--CAGCTCAGCTCGGT	1362

1081	GCCTATCGCTCGGCCACCGGGCATGGGCATCCGGCTGGACGGCGGCACGGCCCTATGCCGGG	1141
1363	GGCGAAATCACCGCACACCTTTGACTCCATGCTGGTGAAAAATGACCTGCCGTGGTTCCGAC	1422
1141	GGCGTCAATCACCGCTATTACGAATCACTCCTCGTGAAGGTGACGGCCTGGGCCCCCAGC	1200
1423	TTTGAACACTGCTGTTGCTGTCGACAGCGCGCGTGTGGCTGAGTTCAACCGTGTCTGGTGT	1482
1201	CCCGAAAAGGCCATCGCGCGGATGGACGGGCGCTGCGCGAGTTCCGATCCGGGGCGTG	1260
1483	GCAACCAACATGGTTTCTTGCGTGCCTGCTGCGGGAAGAGGACTTCACATTCCAAGCGC	1542
1261	GCCACCAACATCGCCTTCGTCGAGAACCTGCTGAAGCACCCGAGTTTCTCGACTATTCC	1320
1543	ATCGCCACCGGATTCATTGCCGATCACCCGACCTCCTTCAGGCTCCACCTGCTGATGAT	1602
1321	TACACGACGAAATTCATCGACACGACGCCGACCTCTTCAACTTCAAGCCGCGTGTGAC	1380
1603	GAGCAGGACGCATCCTGGATTACTTGSAGATGTCAACCGTGATCACCGTGAACAAGCCTC	1656
1381	CGGGCGACGAAGATCCTGACCTACATCGCCGACATCACCCGTGAACGGGACCCCGAGACG	1440
1657	GGTGTGCGTCCAAAGGATGTTGCAGCTCCTATCGATAAGCTGCCCTAAACATCAAGGATCTG	1716
1441	GCCGGCCGGGTCCGCCCTCGGCCGAGCTGAAGGATCCGAAGGCACCCGAGCCCCAAGGC	1500
1717	CCACTGCCACCGCGTTCCCGTGACCCGCTGAAGCAGCTTGGCCCCAGCCGGTTTGCTCGT	1776
1501	GCACCGACGCCCGCACGCGGACCTCTCGAGGAGAAAGGCCCGCGGTGCGCGAC	1560
1777	GATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACTTCCGCGATGCACACCAG	1836
1561	TGGATGGCCCGCAGACCCCGTGTGATGACCGACACGACGATGCCGACGGCCACCAG	1620
1837	TCTTTGCTTGGACCCGAGTCCGCTCACTCGCACTGAAGCCTGCGGCAGAGCCGTGCGA	1896
1621	AGCTTGTCTGCCACCCGGATGCGCTCGATCGACATGATCAAGGTACGCCCGCCTATGCG	1680
1897	AAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCCTGGGGCGCGCAGCCTACGATGTGGCG	1956
1681	GCGAACCTCGCGGCCCTCTTCTCGTGGAAATGCTGGGGCGCGCCACCTTCGATGTGGCC	1740
1957	ATGCGTTTCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGGAGGCGATGCCG	2016
1741	TATCGCTTCTCGAGGAATGTCCCTGGCAGGGCTGCGCGACATCCGCGCCCGCTGCC	1800
2017	AATGTAAACATTACAGATGCTGCTTCGCGCGCGCAACACCGTGGGATACACCCCGTACCCA	2076
1801	AACGTCAATACGACAGATGCTGCTGCGCGCTCGAACGGGTGCGCTATACGAACTACCCC	1860
2077	GACTCCGTCTGCCGCGGTTTGTAAAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGC	2136
1861	GACAATGTGGTGCAGGAATTCGTCGCTCAGGGCGCGAAACCGGCGTCGACGTGTCCGC	1920
2137	ATCTTCGACCGGCTTAACGACGCTCTCCAGATGGTCCAGCAATCGACGAGTCTCTGGAG	2196
1921	GTGTTGCACTCGTCAACTGGTTCGAGAACATGCGCGTGGCAATGGATGCGGTGATCGAG	1980
2197	ACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAAT	2256
1981	GCCAAACA--AGTCTCGAGGGGACCGATCTGCTACACGGGCGACCTGCTCGATCCCGAC	2037
2257	GAAAAGCTCTACACCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGC	2316
2038	CGCTCCAAATACGATCTGAACACTACTATGTCCGCAATGGGCCCGCGCTGCCGACGCGGGC	2097
2317	GCTCACATCTTGGCCATTAAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCGGTAAACCAAG	2376
2098	GCGCATGTCTGGGTCTGAAGGACATGGCCCGGGCTCTGAAGCCTGCCGCCCGCGGTG	2157
2377	CTGGTCAACCGCACTGCCCGGTGAATTCGATCTGCCAGTGCACGTGCACACCCACGACACT	2436
2158	CTGGTGAAGGCGCTGAAGGAGGAGGTGGGCCCTGCCGATCCACTTCCACACCCACGACAG	2217

QY	2437	GCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGAC	2499
Db	2218	AGCGGAATTGCGGCGCGACCGTGCTCGCCGCTTCGCGATGCCGGGTGGATGCCGTGCGAT	2277
QY	2497	GGTGCTCCGCAACCACTGTCTGGCAACCACTCCAGCCATCCCTGTCTGCCATTGTTGCT	2556
Db	2278	GCGGCGATGGACGCCCTTCTCGGCGGCACTTCGACGCCCTGCCCTCGGCTCGATCGTCGAG	2337
QY	2557	GCATTCCGCGCACACCCGTCGCGATACCGGTTTGACCTCGAGGCTGTTTCTGACCTCGAG	2616
Db	2338	GCGCTGAAGCACACCGACCGCGACACCGGCCCTCGACATCGCGCGATCCGCGAGATCTCG	2397
QY	2617	CCGTACTGGGAAGCAGTGGCGGCACTGTACTCTGCCATTGAGTCTGGAAACCCAGGCCCA	2676
Db	2398	GACTACTGGGGCCATGTGGCCACGAGTATTCGGGCCCTTCGAATCGGGCCCTGCCCTCGCCC	2457
QY	2677	ACCGTTCGCGTCTACCGCCACGAAATCCAGCGCGACAGTTGTCCAACTGCGTGCACAG	2736
Db	2458	GCCTCCGAGGTTCTATCTGCACGAGATGCCCGCGCGCAGTTTCAACCACTCAAGGCGCAG	2517
QY	2737	GCCACCGCACTGGGCGCTTCGCGATCGTTTCGAACCTCATCGAAGACAACTACGAGCGGTT	2796
Db	2518	GCGCGCTCCAATGGGGCTCGAGGAACGCTGGTCCGAGTGGCGCAGGCCCTATGCCGACGCG	2577
QY	2797	AATGAGATGCTGGGACGCCCAACCAAGGTCAACCCATCTCTCCAAGGTTGTTGGCGACCTC	2856
Db	2578	AACCGGATGTTTCGGCGACATCGTGAAGGTCAACGCCCTCGTTCGAAGGTGGTGGCGACATG	2637
QY	2857	GCACTCCACCTCGTTGGTGCGGTTGTGGATCCAGCAGACTTGTGTCGCCGATCCACAAAAG	2916
Db	2638	GCGCTGATGATGGTGGCGCAGGGGCTGACGCGGAAGAGGTTCGAGGATCCCGAGGTGCGAG	2697
QY	2917	TACGACATCCAGACTCTGTGCATCGCGTTCTTCGCGCGGCGAGCTTGGTAACCTCCAGGT	2976
Db	2698	GTGAGCTTCCCGACTCGGTCTGGACATGCTCAAGGGCAATCTCGGCCAGCCCCACGGC	2757
QY	2977	GGCTGGCCAGAGCCACTGCGCACCCGCGCACTGGAAGGCGGCTC-----	3020
Db	2758	GGCTGGCCCGAGCCGATCTCTGAAGAAGGTGCTGAAGGCGAGGCACCCTCGACCGAGCGA	2817
QY	3021	-----CGAAGGCAAGGCACCTCTGACGGAAGTTCTCTGAG	3054
Db	2818	CCGGCGCGCATCTGCCGCCCGCTCGACATCGCAGCCGCGCGCGAGAGCTCCTGTGCGAG	2877
QY	3055	GAAGAGCAGGCGCACCTCGACGCTGATGATTTCCAAGGAACGTTCGCAATAGCCTCAACCG-	3113
Db	2878	ATCAAGCAGGGCGACGACGATCCGCTCGACACGGCCGTCGATGCCAGGATCTGAACGGC	2937
QY	3114	--CCTGCTGTTCCCGAAGCCCAACGAAGATTCTCTCGAGCACCGTCGCCGCTTCGGCAAC	3171
Db	2938	TACCTCATGTATCCCAAGTCTTACCGACTACCCGCGCCGCCACAGGATCTACGGGCGG	2997
QY	3172	ACCTCTGCGCTGATGATCGTGAATTCTTCTACGGCCCTGGTTCGAAGCCCGCGAGACTTTG	3231
Db	2998	GTGCGGACGCTGCCGACCCCGACCTTCTTCTACGGGATGGACCGGGCGAGGATCTCG	3057
QY	3232	ATCCGCCCTGCCAGATGTGGCACCCCACTGCTTGTTCGCCCTGGATGCGATCTCTGAGCCA	3291
Db	3058	GCCGAAAT--CGACCCCGCGCAAGACGCTCGAGATCCGGCTGTCCGCCGTGGCGGAGACG	3114
QY	3292	GACGATAAGGGTATGCGCAATGTTGTGGCCCAACGTCAACGGCCAGATCCGCCCAATGCGT	3351
Db	3115	TCGGACGACGGCGATGCCAAGGTGTTCTTTCGAGCTGAACGGCCAGCCCGCGGTGATCCGC	3174
QY	3352	GTGCGTGACCGCTCCGTTGAGTGTGTCAACCGCAACCGCAGAAAGGCAGATTCTCTCCAAC	3411
Db	3175	GTGGCCAAACCGGGCGGTGAAGGCCCAAGACCCGCGACCCCGGCCCAAGGCGCAGGACGGCAAT	3234
QY	3412	AAGGGCCATGTTGCTGCACCAATTCCGCTGGTGTGTCAAC--GTGACTGTTGCTGAAGGT	3468
Db	3235	CCGGCCCATGTCCGGCGCCCGCATGCCGGTTCCGTCGCTCGCTCGGTCGCGGTCTCGGCGGGC	3294

QY	3469	GATGAGGTCAAGGTCGAGATGCAGTCGCAATCATCGAGGCTATGAAGTGAAGCAACA	3528
DB	3295	CAGAAGGTGAAGCCGGCGCATCTCCTCGTCACCATCGAGGCGATGAAGATGGAGACCGGG	3354
QY	3529	ATCACTGCTTCTGTTGACGGCAAAATCGATCGGTTGTGGTTCTCTGTCGAACGAAGGTG	3588
DB	3355	CTCCATGCCGACCGTGGCGCCACCGTGAAGGCTGTCCATGTGCGGGCCCGGCGGCAGATC	3414
QY	3589	GAAGGTGGCGACTTGAT	3605
DB	3415	GAGCGAAGGACCTGCT	3431

RESULT 13
 US-10-369-493-35714
 ; Sequence 35714, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 35714
 ; LENGTH: 3459
 ; TYPE: DNA
 ; ORGANISM: Mesorhizobium loti
 US-10-369-493-35714

Query Match	17.8%;	Score 643.6;	DB 15;	Length 3459;
Best Local Similarity	51.6%;	Pred. No. 8.7e-186;		
Matches 1788; Conservative	0;	Mismatches 1599;	Indels 75;	Gaps 11;

QY	229	GCATTCAAAAAGATCTTGCTAGCAAAACCGCGGAAATCGCGTCCGTGCTTTCCGTGCA	288
Db	4	GCATCACGAAGATCCTCGTCGCAACCGGTCAAGAAATCGCCATCGCGTCTTTCCGCGG	63
QY	289	GCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCCGTGAAGATCGGGATCATTC	348
Db	64	GCCAATGAACCTGGGCCTCAAAAACCGTGGCGATCTGGGCGAGGAAGACAAATATTCGCTG	123
QY	349	CACCGCTCTTTTGTCTCTGAAGCTGTCCGCATTTGGTACC-----GAA	390
Db	124	CACCGCTTCAAGCCGACGAGAGCTACCAGGTCGGGCGCGTCCGCATCTCACC AAGGAT	183
QY	391	GGCTCACCAAGTCAAGGCGTACCTGGACATCGATGAAATTAATCGGTGCAGCTAAAAAGTT	450
Db	184	ATGGGCGCGATCGAGAGCTATCTGTGATCGAGGAGTGATCGCGTCGCCGGCTCTCG	243
QY	451	AAAGCAGATGCCATTTACCGGGATACGGCTTCTGTCTGAAAATGCCAGCTTGCCCGC	510
Db	244	GGCGCGGATGCCATCCACCCCGCTACGGGCTTCTGTCCGAAAAGCCCGAATTCGCCGAA	303
QY	511	GAGTGTGCGGAAAACGGCATTACTTTTATTGGCCCAACCCACAGAGTTCTTGATCTCACC	570
Db	304	GCCTGCGGCAAGCGGGCATACCTTTCATCGGGCCGAGCGGACACGATCGCGCCGCTC	363
QY	571	GGTGATAAGTCTCGCGGGTAAACCGCCGGAAGAAGGCTGGTCTGCCAGTTTGGCGGAA	630
Db	364	GGCAACAAGGTGCGGGCGCGCAATCTCGCCATCGAGGTGCGCGTGCTGTATTTCCCGCC	423
QY	631	TCCACCCC--GAGCAAAAACATCGATGAGATCGTTAAAACCGCTGAAGGCCAGACTTAC	687
Db	424	ACCGATCCGTTCCGACGATATGGAGGCGGTCAAGAACTGGCCAAGGAGATCGGCTAT	483

QY 688 CCCATCTTTGTGAAGCAGTTGCCGGTGGTGGCGGACGCGGTATCGGTTTGTGTCTTCA 747
Db 484 CCAGTGATGCTCAAGGCTCCTGGGGCGCGGTGGGCGGCGATCGCGCCATCCGCTCC 543
QY 748 CCTGATGAGCTTCGCAAAATTAGCAACAGAAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGC 807
Db 544 GAGGCCGATCTCGCCCGTGAGGTCAAGGAAAGCGGAGCGGAAAGCGCCTTCGGC 603
QY 808 GATGGCGGGTATATGTCGAACGTTGCTGTGATTAACCTCTAGCATATTAAGTGCAGATC 867
Db 604 AAGGACGAGGTCTATCTCGAAAAGCTGATCGAGCGCGCCCGCCACGTCGAGGTGCAGGTG 663
QY 868 CTTGGCGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT 927
Db 664 CTTGGCGACACGATGSCAATGCCGTGACCTTGTGAGCGCGACTGTCTGATCCAGCGC 723
QY 928 CGTCACCAAAAAGTTGTCGAAATTGCGCCAGCACAGCATTTTGGATCCAGAACTGCGTGAT 987
Db 724 CGCAACGAGAGTCTGTCGAGCGGGCGCGCGCCCTTATCTCGAAATGTGCGAGCGCGAG 783
QY 988 CGCATTTGTGCGGATGTCAGTAAAGTTCTGCGCTCCATTGGTTACAGGGCGCGGAAACC 1047
Db 784 GAGCTTTGCGGCTACGCGCTGAAGATCGCGCGGAGACCACTATATCGCGCGCGGACG 843
QY 1048 GTGGAATTTCTTGGTCCGAT--GAAAAGGGCAACCACTCTTTCATCGAAATGAACCCACGT 1104
Db 844 GTCGAGTTCTGCGAGATGCCGATACCGGAAAATTCTATTTTCATCGAGGTCAACCCGCGC 903
QY 1105 ATCCAGGTTGAGCACACCGTGAAGTGAAGAACTCACCGAGGTGGACCTGGTGAAGGCGCAG 1164
Db 904 ATCCAGGTCGAGCATACCGTCAACGAGCAGGTGACCGGCATCGATATCGTCAAGGCGCAG 963
QY 1165 ATGGGCTTGGCTGCTGTCGCAACCTTGAAGGAATTG-----GGTCTGACCCCAAGAT 1215
Db 964 ATCCACATCTCGACGGCTTCGCCATCGGCACACCGCAATCGGGCGTCCGGCGCAGAAG 1023
QY 1216 AAGATCAAGACCCAGGTGACGACTGCGTGGCGGAAATCAACCGGAAGATCCAAACAAC 1275
Db 1024 GATATCAGGCTGAACGGCCATGCCCTTGAGTGGCGCATCACCAACGAGGATCCGAGCAC 1083
QY 1276 GGCTTCGCCCCAGATACCGGAACATATCAACCGGTACCGCTCAACGAGCGGAGCTGGCGTT 1335
Db 1084 AATTTTCATCCCGGACTATGGCGCGCATCACCGCTATCGCGGCGCCACCGGCTTCGGCATC 1143
QY 1336 CGTCT--TGACGGTGCAGCTCAGCTCGTGGCGGAAATCAACCGCACTTTGACTCCATG 1392
Db 1144 CGGCTGATGGCGGACCGCCTATTCTGGCGCGGTCAATCACCGCTTCTACGATCCGCTG 1203
QY 1393 CTGGTGAATAATGACCTGCGGTGGTTCCGACTTTGAAACTGTGTTGCTGTCGTGCACAGCGC 1452
Db 1204 CTGGAGAAGGTGACGGCGTGGGCGCCGACGCGCGCGGAGACCAATTGCGCGCATGAACCCG 1263
QY 1453 GCGTTGGCTGAGTTACCGTGTCTGGTGTGTAACCAACATGTTGTTCTTCTGCGTGGTTG 1512
Db 1264 GCGCTGCGGAAATTCGCGATTCGCGGCTTGGCCACCAACCTCACTTCTCGAAGCGATC 1323
QY 1513 CTGCGGGAAGAGGACTTCACTTCCAAGCGGATCGCCACCGGATTCATGCGGATCACCCG 1572
Db 1324 ATCAACCAACCGAGCTTCGCGGACAAATTCCTACAGCAACCAAGTTTCATCGACACGACGCG 1383
QY 1573 CACCTCCTTCAGGCTCCACCTGCTGATGATGAGCAGGAGCGCATCTCTGGATTACTTGGCA 1632
Db 1384 GAGCTGTTCCAGCAGGTCAAGCGGACGAGGACCGCGCGACCAAGTGTCTCAACTATCTGGCC 1443
QY 1633 GATGTACCGGTGAACAAGCCTCATG-----GTGTGCGTCCAAAGGATGTTGCAGTCTCT 1686
Db 1444 GATGTACGCGTCAACGGCCATCCGAGACGCGCGGCGCGCCGACGCGGAAAGCGCGATGCG 1503
QY 1687 ATCGATAAGCTGCCATAACATCAAGGATCTGCCATGCGCACGCGGTTCCCGTGACCGCCTG 1746
Db 1504 GCCGCACCGGTGCTGCCCTATCTCAACGGCAATGTGCGGGCGGCGAGCAAGCAGAGCTG 1563
QY 1747 AAGCAGCTTGGCCCCAGCGCGGTTTGCTCGTGTATCTCCGTGAGCAGGACGCACTGGCAGTT 1806

Db 1564 GACGTGCTCGGTCCGAAAAAATTCGCCGCTGGATGCGGAAACAAAGCAAGTTCTGGTC 1623
QY 1807 ACTGATACCACTTCGCGCATGCACACAGTCTTTTGTGCGACCGGAGTCCGCTCATTC 1866
Db 1624 ACCGATACGATGCGCGACGCGGCACACAGTCTGCTCGCGACGCGCATGCGCAC 1683
QY 1867 GCACTGAAGCCTGCGGCGAGAGCCGTGCAAAAGCTGACTCCTGAGCTTTTGTCCGTGGAG 1926
Db 1684 GACATTGCCAATATTCCCGCACCTATGCGCGCGCCCTGCGCGAGCTTCTGTCTCGTAA 1743
QY 1927 GCCTGGGCGCGCGACCTACGATGTGGCGATGCGTTTCTCTTTAGGATCCGTGGGAC 1986
Db 1744 TGCTGGGCGCGCGACCTTCGACGTCGCGATGCGCTTCTTACCAGGATCCTTGGGAG 1803
QY 1987 AGGCTCGACGAGTGGCGGAGCGCATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGC 2046
Db 1804 CGGCTGTGCTGCTGCGCGAGGCGCGCCAACTGTGTGTCAGATGCTGCTGCGCGGC 1863
QY 2047 CGCAACACCGTGGGATACACCCCGTACCCAGACTCCGTCTGCCGCGGTTTGTAAAGAA 2106
Db 1864 GCCAACGGCGTTCGTTACACCAATTTATCCGACAAATGTCTGTCAGCATTTCTGTCRAGCAG 1923
QY 2107 GCTGCCAGTCCGCGGTGGACATCTTCGATCTTCGCGATCTTCGACGCGGTAAACGACGCTCTCCAG 2166
Db 1924 GCGCGAGCGCGGTATCGACCTGTTTCCGCTCTTCGACTGCTGAACTGGGTGAGAAC 1983
QY 2167 ATGCGTCCAGCAATCGACGCGAGTCTTCGAGACCAACACCGCGGTAGCGGAGGTGGCTATG 2226
Db 1984 ATGCGGTGCGCCATGAGCGCGGTG---GGCGCGAAGGCAAGCTGATCGAAGCGCGATG 2040
QY 2227 GCTTATTCTGTGATCTCTGATCCAAATGAAAAGCTCTACACCTGGATTACTACCTA 2286
Db 2041 TGCTACACCGCGACATCTCGATCCGCGCGGGGCCAAATACGATCTGAAATATTATGTC 2100
QY 2287 AAGATGGCAGAGGAGATCGTCAAGTCTGCGCTCACATCTTGGCCATTAAGGATATGGCT 2346
Db 2101 GGCTTGGCCAGCGAATTGACGGCGCGCGCGCCACATCATCGCCGTCAAGGACATGGCC 2160
QY 2347 GGTCTGCTTCGCCAGCTGCGGTAAACCAAGCTGGTCAACCGCATGCGCGCTGAATTTCGAT 2406
Db 2161 GGCTGTTGAAGCGCGCGCGCGCTGCTGTTCAAGGCGCTGCGGAGGCGGACCGAC 2220
QY 2407 CTGCCAGTGCAGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCT 2466
Db 2221 CTGCCGATCCATTTCCATACCCACGACACGCTGCGCCTGTGCGCGCGACCGTCTGCTGGCG 2280
QY 2467 GCAGCTCAAGCTGCTGCAGATGCTGTTGACGGTCTTCCGCAACCACTGTCTGGCACCC 2526
Db 2281 GCGGTTGAGAGCGCGTGCAGCCATCGATCGGCGATGAGCGCTTCTCGGCAACACG 2340
QY 2527 TCCAGCCATCCCTGTCTGCCATTGTTGCTGCAATTCGCGCACACCCGTTCGCGATACCGGT 2586
Db 2341 TCGCAGCCTTGCCTGGGCTCGATCGTCGAGCGCTGAAGGSCACCGAGCGCGACCCGCGC 2400
QY 2587 TTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCAGTGGCGGACTGTAC 2646
Db 2401 CTCGACCCGCAATGGATCCGCAAGATCTGTTCTACTGGGAAGCGGTGGCAACCGATAC 2460
QY 2647 CTGCCATTTGAGTCTGGAACCCCGAGCCCAACCGGTGCGCTCTACCGCCACGAAATCCCA 2706
Db 2461 GCCGCTTCGAAACGACCTCAAGGGCGCGCTTCGGAAGTCTACTGCTGATGAAATGCCG 2520
QY 2707 GCGGACAGTTGTCCAACTGCGTGCACAGGCCACCGCACTGGGCTTTCGGATCGTTTC 2766
Db 2521 GCGGACAAATTCACCAACCTCAAGGAGCAGGCGCGCTGCTCGGGGTGGAACGCGCTGG 2580
QY 2767 GAACTCATCGAAGACAACTACGCGCGGTTAATGAGATGCTGGGACGCCCCAACCAAGGTC 2826
Db 2581 CATGAGGTGGCGACACCTATCACGACGCTCAATCTGATGTTTCGGCGACATCGTCAAGGTG 2640
QY 2827 ACCCATCTCCAGGTTGTTGGCGACCTCGCACTCCACCTCGTTGGTGGGTGTGGAT 2886

Db 2641 ACGCCGTCATCCAAAGGTCGTGCGGCACATGGCCCTGATGATGGTCAGCCAGGACCTGACC 2700
QY 2887 CCAGCAGACTTGTCTGCGGATCCACAAAAGTACAGACATCCAGACTCTGTCTATCCGGTTC 2946
Db 2701 GTCGCCGATGTCGAAACCCCGCCAGGATATTGCTTCCCGACTCGGTGCTGATG 2760
QY 2947 CTGCGCGCGAGCTTGTAACCTCCAGGTGGCTGGCCAGAGCCACTGCGCACCCGCGCA 3006
Db 2761 CTGCGCGCGATCTCGCCAGTCGCCGCGGTGGCCCGCGGCTGCGAGAAAGCGG 2820
QY 3007 CTGGAAGCGCGCTCCGAAGGCAAGGCACTCTGACGGAAGTTCCTGAGGAAGAGCAGCGG 3066
Db 2821 CTGAAAGCGCAGCAGCGGATCACCGCAGCGCCAGGCTCGCTCAAGCCCGCGATCTC 2880
QY 3067 CACCTCGACGCTGATGATTCGAAGGAAGCTCGCAATAG-----C 3105
Db 2881 AAGGCCAGCGCAAGGAGATCGAGGAAGCTCGAGCGCAAGCTCTCGGAATACGAATTC 2940
QY 3106 CTCAACCGCGCTGCTGTTCCGGAAGCAACCGAAGATTCCTCGAGCACCGTCGCGCTTC 3165
Db 2941 GCCTCCTGCTGATGATTCGAAAGGTGTTCACTGACTTCGCGCGCGCAGGAACCTAC 3000
QY 3166 GGCAACACCTCTGCGCTGGATGATCGTGAATCTTCTACGCGCTGGTCGAAGCGCGGAG 3225
Db 3001 GGCCCGGTGAGCGTCTGCGGACCGGACCTATTTCTACCGCATGAAATCGGAAGACGAG 3060
QY 3226 ACTTTGATCCGCTGCCAGATGTCGCGACCCCACTGCTGTTGCTGCTGATGCGATCTCT 3285
Db 3061 ATCTTCATCGACAT---CGAGAAAGGTAAAGACGCTGGTCTGCGGTGCTTGGCATCGGC 3117
QY 3286 GAGCCAGACGATAAGGATGATGCGCAATGTTGTGGCCAACTGCAACGGCCAGATCCGCCCA 3345
Db 3118 GATGTGACGACAAGGGCATGGTCACGGTGTCTTCGAGCTCAACGGCCAGCCACGGCGC 3177
QY 3346 ATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAA---AAGGAGAT 3402
Db 3178 GTGAAGGTGCGGACCGGCGCATGCGGCGCTCCGCGCGCAAGCGCGCGCTTAAGGCGGAG 3237
QY 3403 TCCTCCAAAGGGCCCATGTTGTGTCACCATTCGCTGTTGTTGTACCGTGACT---GTT 3459
Db 3238 CCTGGCAAGGCGCATGTGCGCGCGCGCATGCGGCGCGGCTGCTGCTGCTGCTGCTGCTG 3297
QY 3460 GCTGAAGGTGATGAGGTCAAGGCTGAGATGCGATCGCAATCATCGAGGCTATGAAGATG 3519
Db 3298 GCCACGGGCAAGCGGTGAAGCGCGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3357
QY 3520 GAAGCAACATCACTGCTTCTGTTGACGGCAAAATCGATCGCGTGTGTTCTCTGCTGCA 3579
Db 3358 GAAACGGCGTGCATGCCGAGCGGTGACGGCACCGTCCGCGGCGGCTGCTGCTGCTGCTGCTG 3417
QY 3580 ACGAAGGTGAAGGTGGGAGCTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3621
Db 3418 GACCAGATCGATGCCAAGGATCTGCTGATAGCTTCCGCTTGA 3459

RESULT 14

US-10-369-493-35137
; Sequence 35137, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 35137
; LENGTH: 3441
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-35137
Query Match 17.0%; Score 617; DB 15; Length 3441;
Best Local Similarity 51.6%; Pred. No. 1.2e-177;
Matches 1776; Conservative 0; Mismatches 1590; Indels 75; Gaps 13;
QY 238 AAGATCTTGGTAGCAACCCGCGCGCAAAATCGCGTCCGTCTTCCGTGACGACTCGAA 297
Db 7 AAATACTTGTGCCAAACCGATCCGAAATTCGATCCGCTTTCGGGCGAGCAACGAG 66
QY 298 ACCGTGCGAGCCACGGTAGTATTTACCCCGTGAAGATCGGGGATCATTCACCGCTCT 357
Db 67 CTTGGGATCAAAACCGTTGCGATTTGGGCGGAAGAGCAAGCTGTCTTTGCACCGCTTC 126
QY 358 TTTGCTTCTGAAGCTGTCCGCAATGGTACC-----GAAGGCTCACCA 399
Db 127 AAGCGGATGAATCCTATCAGGTCCGACGGGTCCGATCTCGCAAGGATATGGGACCG 186
QY 400 GTCAAGCGGTACCTGGACATCGATGAAATATCGGTGACAGCTAAAGATTAAAGCAGAT 459
Db 187 ATCGAGAGTTATCTTTTCGATCGAGGAGGTATCCGCTGTCGCAAGCTCTCCGAGCGGAT 246
QY 460 GCCATTACCCGGGATACGGTTCCTGTCTGAAAAATGCCAGCTTCCCAGGAGTGTGCG 519
Db 247 GCGATCCATCCCGTTATGCTTCTGTCGAAAGCCCTGAGTTCGTGAGGCTTGCAC 306
QY 520 GAAAAAGGCAATTAATTTATGGCCCAACCCAGAGGTCTTGTATCTCACCGGTGATAAG 579
Db 307 AAGGCCGCGCATCACCTTTCATCGGCGCGACACCGGACACGATGCGCCAGCTCGGCAACAAG 366
QY 580 TCTCGCGGTAAACCGCGCGCAAGAAAGCTGTCTGCCAGTTTGGCGGAATCCA---CC 636
Db 367 GTCGCCGCGCAATCTGCGGATTTGCTGTTGATGTCCCGTGTTCGCCACCAATCCT 426
QY 637 CCGAGCAAAAAACATCGATGAGATCGTTAAAGCGCTGAAGCGGCTTTCGGCGATGCGCG 696
Db 427 CTGCTGACGATATCGCGAAGTGGAGCGTATGGCCGAGGAAATCGGTTATCCCGTCATG 486
QY 697 GTGAAGSCAGTTCCCGGTGTCGCGGACGCGGTATGCTGTTTGTGTTTTCACCTGATGAG 756
Db 487 CTCAAGGCTCCTGGGCGCGGTGGCGCGCATGCGCGCCATTCGCAAAAAGGAAGAT 546
QY 757 CTTCGCAAAATAGCAACAGAGCATCTGTAAGCTGAAGCGGCTTTCGGCGATGCGCGCG 816
Db 547 CTCGCCCGTGAGGTGACGGAAGCAAGCGCGAGGCGAAGCGCGCTTCGGCAAGGACGAG 606
QY 817 GTATATGTCGAACGCTGCTGTGATTAACCTCAGCATATTGAAGTGCAGATCCTTGGCGAT 876
Db 607 GTTTATCTGAAAGCTCGTCGAGCGCGCCCGCCATGTGAGAGCCAGATTCTCGGCGAT 666
QY 877 CACACTGGAGAGTTGTACACCTTTATGAACGTGACTGCTCACTGCGCTCGTCACCAA 936
Db 667 ACGCATGSCAATGTCTGTCATCTGTCGAGCGGGATTGTTGATCCAGAGACGCAATCAA 726
QY 937 AAAGTTGTCGAAATTGCGCCAGCAGCATTTGGATCCAGAACTGCGTGATCGCATTTGT 996
Db 727 AAGTCTGTCGAGCGCGCGCAGCAGCATCTGTCCGAAGCGCGAGCCAGGAACCTGGCC 786
QY 997 GCGGATGCAAGTAAGTTCTGCGCTCCATTGGTTACCGGCGCGGGAACCGTGGATTTC 1056
Db 787 GCCTATTCCTGAAGATCGGAGCGCGGACCAACTACATCGGCGCGGCACTGTGCAATAT 846
QY 1057 TTGGTCTGAT---GAAAAGGGCAACCACTGCTTTCATCGAAATGAACCCAGTATCCAGTT 1113
Db 847 CTGATGGATGCCGATACCGGCAAAATTTCTACTTCATCGAGGTCAATCCGCGTATCCAGGTG 906
QY 1114 GAGCACCGGTGACTGAAGAGTCAACCGAGGTGGAACCTGGTGAAGGCGCAGATGCGCTTG 1173
Db 907 GAGCATACCGTTACCGAAGTCTGTGACCGGCGATCGATATCGTCAAGGCGCAGATCCATATT 966

Qy 1174 GCTGCTGGTGCAACCTT-----GAAGGAATTGGTCTGACC----CAAGATAAGATCAAG 1224
Db CTGGAAGGAGCGGCCATCGGCAACGGCGGAATCCGGGTGCCAAGCAGGAAGATATCCGC 1026
Qy 1225 ACCCAGCGTGACGACTGCGAGTCCGCGATCACCACGGAAGATCCAAACAACGGCTTCCGC 1284
Db 1027 CTCAACGGCCATGCGCTGCGAGTCCGCGATCAGACGGAAGACCCCGGAACAAATTTCAAT 1086
Qy 1285 CCAGATACCGGAACATACCGCGTACCGGTACCGGTACCGGCGGAGCTGGCGTTGCTCTTGAC 1344
Db 1087 CCGGACTATGGCCGATTAACCGCCTATCGCTCGGCTTCCGGTTTCGGCATCCGCTCTGGAT 1146
Qy 1345 GGTG---CAGCTCAGCTCGGTGGCGAAATCACCAGCACACTTTGACTCCCATGCTGGTGA 1401
Db 1147 GGGGCAACGTCCTATACCGGCGCGTCAATCACCCTGTTATTACGATCCGCTGCTCGTCAAG 1206
Qy 1402 ATGACCTGCGGTGCTCCGACTTTGAAACTGCTGTTGCTGCTGCGACAGCGCGGTTGSGT 1461
Db 1207 GTCACGGCCTGGCGCGGAGCGGATGAAGCGATCAGCCGATGGATCGCGTTGCGC 1266
Qy 1462 GAGTTCACCGTGTCTGCTGTGTAACCAACATGCTGTTCTTGGCTGGTGTGCTGGCGAA 1521
Db 1267 GAATTCGTATCCCGCGGTGCGACCAACCTGACCTTCTCGAAGCCATCATCGGTCA 1326
Qy 1522 GAGGACTTCACCTCCAGCGCATCGCCACCGGATTCATTGCCGATCACCCGACCTCCCT 1581
Db 1327 GACAGTTTCGCAACACACCTATACGACGCGCTTCATCGATTTCGACGCGGAGTTGTT 1386
Qy 1582 CAGGCTCCACCTGCTGATGATGACGAGGACGATCCTGCTGATTTACTTGGCAGATGTCACC 1641
Db 1387 GCGCAGGTCAAGCGTCAGGACCGCGCCACCAAGCTTCTGACCTATCTGGCCGATGTGACC 1446
Qy 1642 GTGAACAAGCCTCATGGT-----GTGCGTCCAAAGGATGTTGCGAGCTCCTATCGATAAG 1695
Db 1447 GTCAATGGTCAACCCAGAAACCAAGGTCGTGGAAGCCTGCGGACAAAGCGGCAAGCCCC 1506
Qy 1696 CTGCCTAACATCAAGGATCTGCCACTGCCACCGGGTTCGGTGACCCGCTGAAGCAGCTT 1755
Db 1507 ATCGTGCCCTATATCGATGCGCGGACGCTGACGGCACCAAGCAATTCGTGGACAAGCTT 1566
Qy 1756 GGCCAGCGCGTGTGCTGCTGATCTCCGTGACGAGGACGCACTGGCAGTTACTGATACC 1815
Db 1567 GGCCCTAAGGCTTTGCGGACTGGATGCGCAACGAAAGCGCGTGTGTCACGGATACG 1626
Qy 1816 ACCTTCGCGGATGCAACACAGTCTTTGCTTGCAACCGAGTCCGCTCATTCGCACCTGAAG 1875
Db 1627 ACCATGCGCGACGGAACACAGTCTGCTGTGCGCACCCGCTCCGTACCCATGATATCGCC 1686
Qy 1876 CTGCGGCGAGGCGCGTCGCAAGCTGACTCCTGAGCTTTTGTCCGTGGAGCGCTGGGC 1935
Db 1687 CGCGTTGCCAGCGTTTATCCAAAGGCGCTTCCGACGCTTCTGTGCTGGAATGCTGGGC 1746
Qy 1936 GGCGCGACCTACGATGGCGGATGCGGTTTCTTGTGAGGATCCGTGGGACAGGCTCGAC 1995
Db 1747 GGTGCGACCTTCGACGCTCAATGCGCTTCTGACCGGAAGACCCGTGGAGCGCCTGTCA 1806
Qy 1996 GAGCTGCGGAGGCGGATGCCGAATGTAAACATTACAGATGCTGCTTCGGGCGCGCAACACC 2055
Db 1807 CTCATTGCGGAAGGTGCGCGAACCCTGCTGTTGACAGATGCTTCTGCGTGGTGCCAAACGGC 1866
Qy 2056 GTGGGATACACCCCGTACCGAGACTCCGTCTGCGCGCGGTTGTTAAAGGAAGCTGCCAGC 2115
Db 1867 GTCGGTTACAAGAACTATCCGATAAATGTCGTGAAGTATTTCTGCTCCGTGAGGCGCAAGG 1926
Qy 2116 TCCGGCGTGGACATCTTCGCGATCTTCGACGCGCTTAACGACGCTCCCGAGATGCGTCCA 2175
Db 1927 GCGCGCTCGATCTTTTTCGCGCTCTTCGACTGCTGAACTGGGTGGAGAATATCGGGTG 1986
Qy 2176 GCAATCGACGAGTCTTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGCTATTCT 2235
Db 1987 TCGATGGATGCGATTGCCGAGGAGAACA---AGCTCTCGAGGCAACCATCTGCTACACC 2043

Qy 2236 GGTGATCTCTGTATCCAAATGAAGAAGCTCTACACCCCTGGATTACTACCTAAAGATGGCA 2295
Db 2044 GCGGATCTCTTGAATTCGGCACTCCGAAATATGATCTCAATATATATACCAACCTCGCG 2103
Qy 2296 GAGGAGATCGTCAAGTCTGGCGCTCACATCTTTGGCCATTAAAGATATGGCTGCTGCTT 2355
Db 2104 GTCGAGCTGGAAGAGCGCGGCCCATATCATCGCGCTCAAGGATATGGCGGCTGCTG 2163
Qy 2356 CGCCAGCTGCGGTAAACCAAGCTGTTCACCGCACTGCGCCGCTGAATTCGATCTGCCAGTG 2415
Db 2164 AAACCGCGCGCCCAAGGTTCTGTTCAAGCGCTTGGCGAGGCGACCGGTCTGCCGATC 2223
Qy 2416 CACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAA 2475
Db 2224 CACTTCCACACCCATGATACGTCCGGGATTTCCGCCGCGACCGCTTCTTGGCGCGTGGAT 2283
Qy 2476 GCTGGTGCAATGCTGTTGACGGTGTTCGGCACCACTGTCTGGCACCACTCCCGAGCCA 2535
Db 2284 GCCGGCTCGACCGCTCGATGCCGCGATGCGGATGCGCTTCTCCGGCAATACGTGCGAGCCC 2343
Qy 2536 TCCCTGTCTGCCATTGTTGCTGCTGATTCCGGCACACCCCGTGGCATACCGGTTTGGAGCCTC 2595
Db 2344 TGCCTCGGCTCGATCGTGGAGGCGCTCTCCGGATCGGAACCGGATACGGGTCTCGATACC 2403
Qy 2596 GAGGCTGTTTCTGACCTCGAGCCGCTACTGGGAAGCAGTGGCGGACTGTACCTGCCATTT 2655
Db 2404 GAATGGATTGCGCGCATTTCTTCTATTGGGAAGCGTTCGCAATCAATATGCGGCGTTT 2463
Qy 2656 GAGTCTGGAACCCAGGCCCCAACCCGCTCCGCTCTACCGCCACGAAATCCAGGCGGACAG 2715
Db 2464 GAGAGTGACCTCAAGGGCGCTGCCCTCGGAAGTCTATCTGCATGAATGCGGGTGGCCAG 2523
Qy 2716 TTGTTCCAACTGCGTGACAGGCCACCGGCTCCGCTGGGCTTTCGGATTCGTTTCGAATCATC 2775
Db 2524 TTCACCAACCTCAAGGAACAGGCACGTTTCGCTGGGTCTCGAAAGCGCTGGCACGAGGTG 2583
Qy 2776 GAAAGCAACTACGAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCAACCCATCC 2835
Db 2584 GCGCAGGCTATGCGGATGCCAACAGGATGTTTCGGGATATCGTCAAGGTGACGCCGTCC 2643
Qy 2836 TCCAAGGTTGTTGGCGACCTCGCACCTCCACCTCGTTCGTTGGTGGGTTGGATCCAGCAGAC 2895
Db 2644 TCCAAGGTAGTCGGGACATGGCGCTGATGATGTTGAGCCAGGACCTGACGGTGGCCGAT 2703
Qy 2896 TTTGCTGCCGATCCACAAAAGTACGACATCCAGACTCTGTCTATCGGCTTCTGCGCGGC 2955
Db 2704 GTCGAAAACCCCTGACCGTGAAGTGTCTTCCCGGACTCGGTGGTATCGATGCTGAAGGC 2763
Qy 2956 GAGCTTGGTAACCTCCAGGTGGCTGGCGAGAGCCACTGCGCACCCCGGCACTGGAAGGC 3015
Db 2764 GATCTCGGTCAATCGCGGGCGGCTGGCGGAAGCGCTGCAGAAGAGCGCTGAAGGT 2823
Qy 3016 CGCTCCGAAGCAAGCACCTCTGACCGGAAGTTCCTGAGGA-----AG 3058
Db 2824 GAAAAGCCTTACACGTTCTGTCGGGTTTCGCTTCTGGAAGATGCCGATCGATGCCGAA 2883
Qy 3059 AGCAGGCGCACCTCGACGCTGATGATTCCAAAGGAACGTTCGCAATAGCCTCAACCCGC--- 3114
Db 2884 CGGAAGGTGATCGAGACCAAGCTGGAGCGCAAGGTGATGACTTCGAGTTGCTCTCTAT 2943
Qy 3115 CTGCTGTTCCCGAAGCCAAACGAAGATTCTCTACGSCCTGGTGAAGGCCGCGAGACTTTGATC 3174
Db 2944 CTGATGATCCCGAAGGTGTTTACCCGATTTTCGCGCTGACCCCGGAGACATACGCCCGGTC 3003
Qy 3175 TCTGCGCTGGATGATCGTGAATTTCTTCTACGSCCTGGTGAAGGCCGCGAGACTTTGATC 3234
Db 3004 TCCGTGCTGCCACCCATGCCATTTTCTATGSCATGGAGATGGCGAAGAG---CTGTTT 3060
Qy 3235 CGCCTGCCAGATGTGGCACCCCACTGCTTTGTCGCTGGATGCGATCTCTGAGCCAGAC 3294
Db 3061 GCGGATATCGAGCGCGCAAGACGCTTGTCTCATGCTCAATCAGGCTTCGTCGCGCATTGAC 3120
Qy 3295 GATAAGGTTATGCGCAATGTTGTGGCCAAACGTCAACGGCCAGATCCGCCCAATGCGTGTG 3354

Db 3121 GATAAGGCGATGGTGACGGTGTCTTCGAGATCAACGGCCAGCGCGCGCATCAGGTG 3180
QY 3355 CGTGACCGCTCC---GTTGAGTCTGTCAACCGCAACCGCAGAAAAGGCAGATTCTCTCAAC 3411
Db 3181 CCGGATCGCGCCCATGGCGCTTCGGCTCTGCGGTGCGCCGCAAGGCAGAACCCGCAAT 3240
QY 3412 AAGGGCCATGTTGCTGCACCATTCGCTGGTGTGTGCAC---CGTGACTGTTGCTGAAGT 3468
Db 3241 GCGTCCCATATCGCGCGCGCGCATGCCCTGGTGTCTCATCAGCCGGCTCTTCATCAACCGGGT 3300
QY 3469 GATGAGGTCAAGCTGGAGATGCAGTCCGAATCATCGAGGCTATGAAGATGGAAGCAACA 3528
Db 3301 CAGGAGGTCAAGCGCGCGCGACGTGCTCTCGATCGAGGCCATGAAGATGGAACCGCG 3360
QY 3529 ATCACTGCTTCTGTTGACGGCAAAATCGATCGGTTGTGTTCTCTGCTGCAACGAAGGTG 3588
Db 3361 CTGCATGCCGAACCGCAGCGCAAGATCGCTGAAGTCTGTTGAAGCCCGGTGACCGATC 3420
QY 3589 GAAGGTGGCGACTTGATCGTC 3609
Db 3421 GACGCCAAGGATTGTTGATC 3441

RESULT 15

US-10-369-493-38504
; Sequence 38504, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38504
; LENGTH: 3453
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38504

Query Match 17.0%; Score 617; DB 15; Length 3453;
Best Local Similarity 51.6%; Pred. No. 1.2e-177;
Matches 1776; Conservative 0; Mismatches 1590; Indels 75; Gaps 13;

QY 238 AAGATCTTGGTAGCAACCGCGCGGAAATCGCGGTCCGTCTTCCGTGAGCACTCGAA 297
Db 13 AAAATACTTGTGCAACCGCATCCGAAATTGCGATCCGCTTTTCCGGCAGCGAACGAG 72
QY 298 ACCGGTGCAGCCACGGTACGATGAAATATCCCGGTGAAGATCGGGATCATTCACCGCTCT 357
Db 73 CTTGGGATCAAAACCGTTCGATTTGGCGGAAAGAGGACAAGCTGTCTTGCACCGCTTC 132
QY 358 TTTGCTTCTGAAGCTGTCCGCTATGGTACC-----GAAGGCTCACCA 399
Db 133 AAGCGGATGAATCCTATCAGGTTCGGCAGGGGTCCGCATCTCGCCAAGGATATGGGACCG 192
QY 400 GTCAAGGCGTACCTGGACATCGATGAAATATCGGTGCAGCTAAATAAGTAAAGCAGAT 459
Db 193 ATCGAGATTATCTTTTCGATCGAGGAGTTATCCCGTGGCCAAAGCTCTCCGGAGCGGAT 252
QY 460 GCCATTACCCGGGATACGGCTTCTGTCTGAAATGCCAGCTTCCCGCGAGTGTGCG 519
Db 253 GCGATCCATCCCGTTATGCTCTTCTGTCCGAAAGCCCTGAGTTCGTGGAGGCTTCAAC 312
QY 520 GAAAACGGCATTACTTTTATTGGCCCCAACCCCGAGAGGTTCTTGATCTCACCGGTGATAAG 579

Db 313 AAGCCGCGCATCACCTTCATCGGCGCGACACCGGACACGATGCGCCAGTCAACAAG 372
QY 580 TCTCGCGCGGTAAACCGCGCGAAGAGGCTGGTCTGCCAGTTTGGCGGAATCCA---CC 636
Db 373 GTCGCCGCGCGCAATCTGGCGATTTCGGTTGATGTCGCCGTTGTCCCGCCACCAATCCT 432
QY 637 CCGAGCAAAAAACATCGATGAGATCGTTAAAGCGCTGAAGGCCAGACTTACCCCAATCTT 696
Db 433 CTGCTGACGATATCGCGGAAGTGGAGCGTATGGCCGAGGAAATCGTTATCCCGTCATG 492
QY 697 GTGAAGCGCAGTTCCGGTGGTGGCGACCGGATATGCGTTTGTGTTTTCACCTGATGAG 756
Db 493 CTCAAGGCTCTCTGGGCGCGGTGGCGCGCATGCGCGCCATTCGCAAAAAGGAAGAT 552
QY 757 CTTCCGCAAAATAGCAACAGAAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCG 816
Db 553 CTCGCCCTGTGAGGTGACGGAAGCCAGCGGAGGCGAAGSCCGCTTCGGCAAGGACGAG 612
QY 817 GTATATGTGCAACGCTGTGTGATTAAACCTTCAGCATATTGAAGTGCAGATCCTTGGCGAT 876
Db 613 GTTTATCTGGAAGAGCTCGTCGAGCGCGCGCCCATGTGAGAGCGCAGATTCTCGGCGAT 672
QY 877 CACACTGGAGAAATTGTACACCTTTATGAACGTGACTGCTCACTGACGCGTCTGTCACCAA 936
Db 673 ACGCATGGCAATGTCTGTGATCTGTTGAGCGGGATTGTTGATCCAGAGACGAATCAA 732
QY 937 AAAGTTGTGCAAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGT 996
Db 733 AAGTCTGTGAGCGCGCGCCAGCACCCGTATCTGTCGAAGCGCAGCGCCAGGAACCTGGCC 792
QY 997 GCGGATGCAGTAAAGTTCTGCGCTCCATTGTTTACCAGGGCGCGGGAACCGTGAATTC 1056
Db 793 GCCTATTCCCTGAAGATCGCAGCGCGCCAGCAACTACATCGGCGCGCGCACTGTGCAATAT 852
QY 1057 TTGGTTCGAT---GAAAAGGGCAACCGCTCTTCATCGAAATGAACCCACGATCCAGGTT 1113
Db 853 CTGATGGATGCCGATACCGGCAAAATTCTACTTCATCGAGGTCAATCCGCGTATCCAGGTG 912
QY 1114 GAGCACACCGTGAAGAAAGTCAACCGAGTGGACCTGTTGAAGGCGCAGATGCGCTTG 1173
Db 913 GAGCATACCGTTACCGAAGTCTGTGACCGCGCATCGATCGTCAAGGCGCAGATCCATATT 972
QY 1174 GCTGCTGGTGCACCTT-----GAAGGAATTGGGTCTGACC---CAAGATAAGATCAAG 1224
Db 973 CTCGAAGGAGCGCGCATCGGCACGGCGGAATCCGCGGTGCCAAAGCAGGAAGATATCCGC 1032
QY 1225 ACCCACGGTGCAGCACTGCAGTCCCGCATCACACCGAAGATCCAAACAACCGCTTCCGC 1284
Db 1033 CTCAACGGCCATGCGCTGCAGTCCCGCATCACGACGGAAGACCCGGAACACAAATTCATT 1092
QY 1285 CCAGATACCGGAACATATCACCGGTACCGCTCACAGGCGGAGTGGCGTTCTGTTGAC 1344
Db 1093 CCGGACTATGGCCGTATTACCGCTTACCGCTTCCGCTTCCGCTTTCGGCATCCGCTCGAT 1152
QY 1345 GGTG---CAGCTCAGCTCGGTGGCGAAATCAACCGCACACTTTGACTCCATGCTGGTGA 1401
Db 1153 GGGGCGACGTCTTATACCGCGCGCGTCAACCGCTTATTACGATCCGCTGCTCGTCAAG 1212
QY 1402 ATGACCTGCGGTGGTTCGGACTTTGAAACTGCTGTTGCTCGTGACAGCGCGCTTGGCT 1461
Db 1213 GTCACGGCTTGGGCGCGGAGCGGATGAAGCGATCAGCCGATGATCGCGCTTGGCG 1272
QY 1462 GAGTTACCGGTGTCTGGTGTGCAACCAACATTGGTTTCTTGGTGGTGGTGGCGAA 1521
Db 1273 GAATTTGATATCCGCGCGGTTCGACCAACCTTCCGAGCTTCTCGAAGCCATCATCGGTAC 1332
QY 1522 GAGGACTTCACCTCCAGGCGCATCGCCACCGGATTCATTCGCGATCACCCGACCTCCTT 1581
Db 1333 GACAGTTTCCGCAACACACCTATACGACGCGCTTCATCGATTTCGACCGCGGAGTTGTT 1392
QY 1582 CAGGCTCCACCTGCTGATGATGAGCAGGGACCGCATCTGATTACTTGGCAGATGTCACC 1641

Db 1393 GCGCAGGTCAAGCGTCAGGACCGCGCCACCAAGCTTCTGACCTATCTGGCCGATGTGACC 1452
Qy 1642 GTGAACAAGCCTCATGGT-----GTGCGTCCAAAGGATGTTCAGACTCCTATCGATAAG 1695
Db 1453 GTCATATGGTCAACCAGAAACCAAGGGTCTGCGAAGCCTGCGGACAAGCGCGCAAGCCCC 1512
Qy 1696 CTGCCCTAACATCAAGGATCTGCCACTGCGCAGCGGTTCCCGTGACCGCCTGAAGCAGCTT 1755
Db 1513 ATCGTGCCCTATATCGATGCGCGGACGCTGACGGCACCAAGCAATGCTGGACAAGCTT 1572
Qy 1756 GGGCCAGCGCGGTTTGTCTGCTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGTATACC 1815
Db 1573 GGGCCCTAAGGGCTTTGCGGACTGGATGCGCAACGAAAGCGCGTGCTGGTCAACGGATACG 1632
Qy 1816 ACCTTCGGGATGCACACCAAGTCTTTTGTGCTGCGACCGAGTCCGCTCATTGCACTGAAG 1875
Db 1633 ACCATGCGCGACGACACCAAGTCTGCTGCGCCACCGCGTCCGTACCCATGATATCGCC 1692
Qy 1876 CCTGCGGACAGCGCGTGCACAAAGCTGACTCTCCTGAGCTTTTGTCCGTGGAGGCCCTGGGGC 1935
Db 1693 CGCGTTGCCAGCGCTTATTCGAAGGGCGTTCGCGCAGCTTCTGTGCTGGAATGCTGGGGC 1752
Qy 1936 GGC CGCAGCTACGATGTGGCGATGCGTTTCTCTTTGAGGATCCGTGGGACAGGCTCGAC 1995
Db 1753 GGTGCGACCTTCGACGTCTCAATGCGCTTCTGACCGAAGACCGTGGAGCGCCTGTCA 1812
Qy 1996 GAGCTGCGGAGGCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGCGCCGCAACACC 2055
Db 1813 CTCATTCCGGAAGGTGCGCCCGAACCTGCTGTTCAGATGCTTCTGCGTGGTGCCAAACGGC 1872
Qy 2056 GTGGGATACACCCCGTACCCAGACTCCGTCTGCGCGCGCTTTGTTAAGGAAGCTGCCAGC 2115
Db 1873 GTCGGTTACAAGAACTATCCCGATAATGTCTGTAAGTATTTCTGCTCCGTGAGCGGCAAGG 1932
Qy 2116 TCCGGCGTGACATCTTCGCGCATCTTCGACGCGCTTAACGACGCTCTCCAGATGCGTCCA 2175
Db 1933 GCGCGCGTCGATCTTTTTCGCGCTCTTCGACTGCTGAACTGCTGCTGAACTGCTGCGGGTG 1992
Qy 2176 GCAATCGACGCGAGTCTGGAGACCAACACCGCGGTAGCCGAGGTGGGTATGGCTTATTCT 2235
Db 1993 TCGATGGATGCGATTGCGGAGGAGAACAA--AGCTCTCGGAGGCAACCATCTGTACACC 2049
Qy 2236 GGTGATCTCTGTATCCAAATGAAAGCTCTACACCCCTGGATTACTACCTAAAGATGGCA 2295
Db 2050 GCGGATCTCTTGAATTCGGCACGTCGGAATATGATCTCAATATATATACCAACCTCGCG 2109
Qy 2296 GAGGAGATCGTCAAGTCTGGCGCTCACATCTTGCGCCATTAAGGATATGGCTGGTCTGCTT 2355
Db 2110 GTCGAGCTGGAAGAGCGCGCGCCCATATCATCGCGCTCAAGGATATGGCGGCGCTGCTG 2169
Qy 2356 CGCCAGCTGCGGTAAACCAAGTGGTCAACCGCACTGCGCGGTGAATTCGATCTGCCAGTG 2415
Db 2170 AAACCGGCGCGCGCCAGGTTCTGTTCAAGGCGTTCGCGAGGCGACCGGTCTGCCGATC 2229
Qy 2416 CACGTGCACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAA 2475
Db 2230 CACTTCCACACCCCATGATACGTCGGGCAATTCGCGCGGACCGCTTCTTGGCGCGCTGGAT 2289
Qy 2476 GCTGGTGCAGATGCTGTGACGGTGTCTTCGCAACCACTGTCTGGCACCACTCCAGCCCA 2535
Db 2290 GCGGCGTTCGACGCGCTCGATGCGCGGATGGATGCGCTTCTCGGCAATACGTCGACGCCC 2349
Qy 2536 TCCGTGTCTGCCATTTGCTGCAATTCGCGCACACCGCTGCGGATACCGGTTTGAACCTC 2595
Db 2350 TGCTCGGCTCGATCGTGGAGGCGCTCTCCGGATCGGAACGCGATACCGGTCTCGATACC 2409
Qy 2596 GAGGCTGTTTCTGACCTCGAGCCGTAAGGAGGAGTGGCGGACTGTACCTGACCTGCTT 2655
Db 2410 GAATGGATTCGCGCGCATTTCTCTTATTTGGGAAGCGCTGGCAATCAATATGCGGCGTTC 2469
Qy 2656 GAGTCTGGAACCCAGGCCCAACCGGTGCGGTCTACCGCCACGAAATCCAGGCGGACAG 2715
Db 2470 GAGAGTGACCTCAAAGGGCGCTGCTCGGAAGTCTATCTGCAATGAAATGCGGGGTGGCCAG 2529

Qy 2716 TTGTCCAACTCGGTGCAACAGGCCACCGCACTGGGCCCTTTCGGGATCGTTTCGAACTCATC 2775
Db 2530 TTACCAACCTCAAGGAACAGGACAGCTTCGTGGTCTCGAAGCCGCTGGCACGAGGTG 2589
Qy 2776 GAAGACAACACTACGAGCCGTTAATGAGATGCTGGGACGCGCAACCAAGGTCAACCCCATCC 2835
Db 2590 GCGCAGGCTATGCGGATGCCAACAGGATGTTTCGGCGATATCGTCAAGGTGACGCCGTCC 2649
Qy 2836 TCCAAAGTTGTTGGCGACCTCGACTCCACCTCGTTGGTGGGTGTGGATCCAGCAGAC 2895
Db 2650 TCCAAAGTATGTCGGCGACATGGCGCTGATGATGGTGAGCCAGGACCTGACGGTGGCCGAT 2709
Qy 2896 TTTGCTGCCGATCCACAAAGTACGACATCCAGACTCTGTICATCGCGTTCTCTGCGCGGC 2955
Db 2710 GTCGAAACCCCTGACCGTGAAGTGTCTTCCCGACTCGGTGGTATCGATGCTGAAGGGC 2769
Qy 2956 GAGCTTGGTAACCTCCAGGTGGTGGCGCAGAGCCACTGCGCACCCGCGCACTGGAAGGC 3015
Db 2770 GATCTCGGTCAATCGCGCGCGCTGCGCGAAGCGTGCAGAAAGGCGCTGAAGGGT 2829
Qy 3016 CGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCTCTGAGGA-----AG 3058
Db 2830 GAAAAGCCTTACACGGTTCTGTCGGGTTCGCTTCTGGAAGATGCGGATCTCGATGCCGAA 2889
Qy 3059 AGCAGGCGCACTCGACGCTGATGATTCGAAGGAACGTGCGAATAGCCTCAACCGC---- 3114
Db 2890 CGGAAGGTGATCGAGACCAAGCTGGAGCGCAAGGTGATGACTTCGAGTTTGCCTCTAT 2949
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Search completed: March 24, 2004, 06:08:42
Job time : 1227 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 18:35:49 ; Search time 8670 Seconds
(without alignments)
12471.852 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	432.2	11.9	2877	11	AK077665 Mus muscu

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	31	188.4	5.2	1030	29	CNS06M6L	AL405091 T3 end of
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ALIGNMENTS

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DEFINITION	AY408287				
ACCESSION	AY408287.1	GI:39764258			
VERSION	GSS.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 3537)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 3537)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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QY 353 GCTCTTTTGTCTGAAGCTGTCCGCAATGGTACCGAAGGCTCACCAGTCAAGCGGTACC 412
Db 230 GGCAGAAAGCTGTGAAGCCTACCTTATTGGCCGTGGCCTGGACCTGTGACGGCCTACC 289
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QY 473 GATACGGCTTCTGTGAAATATGCCAGCTTCCCGAGTGTCCGGGAAACGCGCATTA 532
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REFERENCE 1 (bases 1 to 3537)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 3537)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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QY 1310 ACCGCTCACAGGCGGAGCTGGCGTTTCTGCTCT---TGACGGTGCAGCTCAGCTCGGTGGCG 1366
Db 1190 TCCGAGCGGAGAGGGCATGGGCATCCGCTCGGATAATGCTTCGCGCTTCCAAGGAGCGG 1249
QY 1367 AAATCACCGCACACTTTGACTCCATGCTGCTGGAATAATGACCTGCGGTGGTCCGACTTTG 1426
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QY 2081 CCGTCTGCGCGCGTTTGTAAAGGAAGTTCAGCTCCGCGTGGACATCTTCCGCTCT 2140
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Db 2030 TTGACTCCCTCAACTACTTGGCCCAACATGCTGTGGGATGAGGCGG---CAGGAAGTG 2086
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QY 2498 GTGCTTCCGCAACCTGCTGGCACCACTTCCAGCCCTCCAGCCATCCCTGCTGCCATGTTGCTG 2557
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Db 2867 ATGGGGGTTCCCGAACCCCTTCGCTCTAAGGTACTGAAGGACC 2911

RESULT 3
AY408286 3537 bp DNA linear GSS 15-DEC-2003
LOCUS Pan troglodytes PC gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY408286
VERSION AY408286.1 GI:39764257
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 3537)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trics
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 3537)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
1..3537
/organism="Pan troglodytes"
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gene

ORIGIN

Query Match 12.2%; Score 442.4; DB 29; Length 3537;
Best Local Similarity 41.5%; Pred. No. 4e-92;
Matches 1004; Conservative 0; Mismatches 1400; Indels 18; Gaps 6;

QY 233 TCAAAAGATCTTGGTAGCAACCGCGCGAAATCGCGTCCGTGCTTTCCGTGAGCAC 292
Db 110 TCAAGANNCTGTTGGCCACAGAGGTGAGATTGCCATCCGTGTGTTCCGGGCTGCA 169

QY 293 TCGAAACCGGTGCAGCCACCGGTAGTATTACCCCGTGAAGATCGGGATCAATCCACC 352
Db 170 CGGAGCTGGGCATCCGCACCGGTAGCCATCTACTGTAGCAGGACACGGGCCAGATGCACC 229

QY 353 GCTCTTTTGTCTGAAGCTGTCGGCATTTGGTACCGAAGGTCCAGTCAAGGGCTACC 412
Db 230 GGCAGAAAGCAGATGAAGCCTATCTCATCGGCGCGCCCTGGCCCCCGTGCAGGCTACC 289

QY 413 TGGACATCGATGAAATTATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTACCCGG 472
Db 290 TGCACATCCAGACATCATCAAGGTGGCCAAAGGAGAACACGTAGATGCAGTACACCTG 349

QY 473 GATACGGTTCCTGTCTGAAATATGCCAGCTTGCCCGGAGTGTGCGGAAACCGGCATTA 532
Db 350 GCTACGGGTTCTCTCTGAGCGAGCGGACTTCGCCAGGCTGCCAGNATGCAGGGTCC 409

QY 533 CTTTATTGGCCCAACCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGGGTAA 592
Db 410 GGTATTATGGGCCAAGCCAGAGTGTCCGCAAGATGGGAGACAAGGTGGAGGCCCGGG 469

QY 593 CCGCCGCGAAGAGGCTGGTCTGCCAGTTTGGCGG---AATCCACCCCGAGCAAAAACA 649

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Db 950 ACGGCAAGCACTACTTTCATCGAGGTCAACTCCCGCTGAGGTGAGCACACCGGTACAG 1009

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QY 1367 AAATCACCGCACACTTTGACTCCATGCTGGTGAATAATGACCTGCGTGGTTCGACTTG 1426

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QY 1427 AAATGCTGTTGCTCGTGACAGCGCGCTTGGCTGAGTTTCAACCGT-----GTCTGGTGT 1481

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Db 1430 NNN 1489

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QY 1662 GCGTCCAAAGGATGTTGACGCTCCTATCGATAAGCTGCCCTAACATCAAGGATCTGCCACT 1721

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QY 2952 CGCGGAGCTTGGTAACCTCCAGGTGGCTGGCGAGCCACTGCGCACCCCGCACTGGA 3011
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RESULT 5
CNS074FW/c
LOCUS
DEFINITION
888 bp DNA linear GSS 07-JUL-2001
clone BA0AB027F04 of library BA0AB from strain CLIB 210 of
Kluyveromyces lactis, genomic survey sequence.

ACCESSION
AL428754
VERSION
AL428754.1 GI:12211948
KEYWORDS
GSS.
SOURCE
Kluyveromyces lactis
ORGANISM
Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

REFERENCE
1 (bases 1 to 888)
Souci t,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
20584711
PUBMED
11152876

REFERENCE
2 (bases 1 to 888)
Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F.,
Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
Genomic exploration of the hemiascomycetous yeasts: 11.
Kluyveromyces lactis
FEBS Lett. 487 (1), 66-70 (2000)
20584721
PUBMED
11152886

REFERENCE
3 (bases 1 to 888)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,

Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES
source
1..888
/organism="Kluyveromyces lactis"
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PYC2 ; pyruvate carboxylase 2]
similar to Saccharomyces cerevisiae ORF YGL062w [PYC1 ;
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misc_feature

ORIGIN
Query Match 6.6%; Score 240.6; DB 29; Length 888;
Best Local Similarity 55.9%; Pred. No. 4.3e-45;
Matches 478; Conservative 0; Mismatches 374; Indels 3; Gaps 1;

QY 395 CACCAGTCAAGGCTACCTGGACATCGATGAAATATCGGTGACGTAAAAAGTTAAAG 454
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QY 575 ATAAGTCTCGCGGGTAAACCGCCGGAAGAGGCTGGTCTGCCAGTTTGGCGGAATCCA 634
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QY 692 TCTTTGTGAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGTTTGTGTTCTTACCTG 751
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Db 435 GTACTTGTTCATTGAAAGATTCTTGGACAAAGCATATCGAAGTTCAATTGTTGG 376
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QY 932 ACCAAAAAGTTGTGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTCGGTGATCGCA 991
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Db 195 AATTCTTAGTCGATAACCAAAACAGACATTACTTTATCGAAATTAACCCAGAAATCAAG 136

Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
Class: transposon-tagged.

FEATURES

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/note="Vector: pHSS6-Sal; A yeast genomic DNA library without 2 micron or mitochondrial DNA was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mTn-3xHA/lacZ minitransposon containing lacZ, URA3, and tet resistance."

ORIGIN

Query Match 6.2%; Score 223.4; DB 28; Length 859;
Best Local Similarity 59.9%; Pred. No. 4.5e-41;
Matches 407; Conservative 0; Mismatches 268; Indels 4; Gaps 2;
QY 827 AACGTGCTGTGATTAACTCCTCAGCATATTGAGTGCAGATCCTTGGCGATCACACTGGAG 886
DB 801 AAAATTCTTGGACAAAGCAAAAGCATATTGAGTTCATTTGTGGCCGATACACCGAAA 742
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DB 682 AAGTGGCNCAGCAAGACTTTACNCCGTGAAGTCGGTGACGCCATTTGACAGATGCAG 623
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DB 502 CAGAAGAAATACCGGTATAGATATTGTGGCGGCTCAGATCCAAATTTGCGGAGGTGCCT 443
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QY 1307 CGTACCGCTACCCAGGCGGAGCTGGCGTTTCGTCTTGACGGTG---CAGCTCAGCTCGGTG 1363
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QY 1364 GCGAATACCCGCACACTTTTGTCTCATGCTGGTGAATGACCTGCCGTGGTTCGGACT 1423
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QY 1484 CAACCAACATTTGGTTTCTT 1502
DB 142 AGACCAACATTTCCCTTCTT 124

RESULT 8

BF251052 637 bp mRNA linear EST 15-NOV-2001
LOCUS EST418309 Coccidioides immitis spherule cDNA library Coccidioides
DEFINITION immitis cDNA clone CIAAB85 5' sequence, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .637

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/lab_host="SOLR"

/clone_lib="Coccidioides immitis spherule cDNA library"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 6.1%; Score 220.2; DB 10; Length 637;
Best Local Similarity 60.4%; Pred. No. 2.2e-40;
Matches 380; Conservative 0; Mismatches 248; Indels 1; Gaps 1;

QY 685 TACCCCATCTTTGTGAGGCGATTTGCCGTTGTGGCGGACGCGGTATGCGTTTGTGCT 744
DB 7 TTTCCCATCATCATCAAGCGCGCTTTCGGCGGCGGTGCGCGGCATGCGTGTCCGC 66

QY 745 TCACCTGATGAGCTTCGCAATATTAGCAACAGATCTCGTGAAGCTGAGCGGCTTTC 804
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QY 805 GCGGATGGCGGCTATATGTCGAACGTCGTGTGATTAACCTCAGCATATTGAAGTGCAG 864
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QY 865 ATCTTTGGCGATCACACTGAGAAAGTTGTACACCTTTATGAACGTCGTCCTACTGCAG 924
DB 187 CTGCTCGCGACAAACCCACGCAACGTCGTCCACCTCTACGAGCGTGAATGCGGTCAG 246

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QY 1045 ACCGTGGAATTTTGGTCGATGAAAAAGGGCAACCCAGCTCTTCATCGAAATGAACCCAGCT 1104
DB 367 ACCGCCGAGTTCTCTCGTCGACCCAGCTCAACCGCTACTACTTTCATCGAGATCAACCCCGC 426

QY 1105 ATCCAGGTTGAGCACACCGTGACTGAAGAAGTACCCGAGGTGGACCTGGTGAAGGCGCAG 1164
|||||
Db 427 ATCCAGGTGAGCACACCATCACCGAGGAGATCACCGGATCGACATCGTCGCCGCCAG 486
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QY 1165 ATGCGCTTGCTGCTGGTGCAACCTTGAAGGAATTGGTCTGACCCCAAGATAAGATCAAG 1224
|||||
Db 487 ATCCAGATCGCGCGCGGCCACCCCTCGAGCAGCTCGGCCTCACCCAGGACCGCATCTCC 546
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QY 1225 ACCCAGGTGCGAGCACTGCGATGCGGCATCACCGGAGAT-CCAAACAACGGCTTCGG 1283
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Db 547 ACCAGAGGCTTCGCCATCCAGTCCGCGATCACCCGAGATCCCAAAAGGGGCTTCCA 606
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QY 1284 CCCAGATACCGGAACCTATCACCGCGTACC 1312
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Db 607 GCCCGACACCGGTAAAGATCGGAGTCTACC 635
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RESULT 9
CA793824
LOCUS
DEFINITION
AGENCOURT 11043532 NICHG_XGC_Emb1 Xenopus laevis cDNA clone
IMAGE:6865891 5', mRNA sequence.
CA793824
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CA793824 862 bp mRNA linear EST 04-DEC-2002
Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 862)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL4488 row: p column: 18
High quality sequence stop: 649.

FEATURES
source
Location/Qualifiers
1..862
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6865891"
/tissue_type="embryo (stage 10)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHG_XGC_Emb1"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
Cloned unidirectionally. Primer: Oligo dt. Average insert
size 1.55 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."

ORIGIN
Query Match 6.0%; Score 216.6; DB 14; Length 862;
Best Local Similarity 56.7%; Pred. No. 1.8e-39;
Matches 421; Conservative 0; Mismatches 319; Indels 3; Gaps 1;

QY 841 AACCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCTT 900
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Db 20 AAACCTCGCCACATTTGAAGTTCAGATACCTCGGTGATAAATATGGAATGTGTACATTG 79
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QY 901 TATGAACGTGACTGCTCACTGCAGCGTCTGTCACCAAAAAGTTTCGAAATTGCCGACGA 960
|||||
Db 80 TATGAAAGAGACTGTTCCGTCAGAGAGGACCCAGAGGTGGTTGAAATAGCCCCAGCT 139
|||||

QY 961 CAGCATTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTAAAGTTCTGCCGC 1020
|||||
Db 140 GCACAGCTGGACCTTCAGCTCAGAGACAGACTGACCCATGACTCTGTAAACTGGCAAA 199
|||||
QY 1021 TCCATTGGTTACAGGGCGCGGGAACCGTGGAAATCTTGTGCGATGAAAAGGCAACAC 1080
|||||
Db 200 CAGGTGGTTATGAGAAATGCCGGCACTGTGGAGTTCTTGTGGATATAACATGGCAAGCAT 259
|||||
QY 1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGAATGAAGAAATGCACC 1140
|||||
Db 260 TACTTCATAGAAGTCAACTCCAGACTCCAAGTTGAGCATACAGTAACGGAAGAAATTACA 319
|||||
QY 1141 GAGGTGACCTGGTGAAGGCGCAGATGCGCTTGGTGTGCTGTGCAACCTTTGAAGGAATTG 1200
|||||
Db 320 GATGTTGACCTAGTCCATGCCCGATCCATGTTGCAGAGGGAAGGCGCTTCTGTGACCTT 379
|||||
QY 1201 GGTCGTGACCCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCGAGTCCCGCATCACCA 1260
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Db 380 GGCCTCAAGCAAGAGAACATCCGTATCAATGGTTGTGCCATTTCAGTGCAGAGTCAACA 439
|||||
QY 1261 GAAGATCCAAACAACGGCTTCGCCCGCAGATACCGGAACATATCACCGCTACCGCTACCA 1320
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Db 440 GAAGACCTTCACGTGGGTTTCAGCCTGATACCTGGTCGGATTGAGGTTTCCGGAGTGA 499
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QY 1321 GGCGGAGCTGGGCTTCTGTTGACGGTG---CAGCTCAGTCTGGTGGCGAAATCACCGCA 1377
|||||
Db 500 GAAGGAATGGGAATCCGACTAGACAGTCTTCAGCTTTTCAAGGAGTGTCTATTTCCCCA 559
|||||
QY 1378 CACTTTGACTCCATGCTGGTGAATGACCTGCCGTGTTCCGACTTTGAAACTGCTGTT 1437
|||||
Db 560 CATTATGACTCCTTCTGTTCAAGGTTATTGCACACGGAAGACCATCAAGTTGCCGCC 619
|||||
QY 1438 GCTCGTGACAGCGCGCTTGGCTGAGTTTACCGTGTCTGTTGTGCAACCAACATTTGT 1497
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Db 620 ACAAAAATGACAGAGCTTTGGCAGAGTTCGGATTAGGGGTGTTAAAGACAATATTTCCC 679
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QY 1498 TTCTTGGCTGCTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATGCCACCGGATTC 1557
|||||
Db 680 TTCTGCAAAAACGCTTTGAAACAATAATCAGTTTCTCCATGGTACAGTACACACTCAGTTT 739
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QY 1558 ATTGCCGATCACCGGCACCTCCT 1580
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Db 740 ATTGATGAAAATCCAGACCTCTT 762
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RESULT 10
AII09467
LOCUS
DEFINITION
GH08678.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH08678 5prime, mRNA sequence.
AII09467
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AII09467 675 bp mRNA linear EST 19-APR-2001
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 675)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: 86 row: G column: 6
High quality sequence stop: 588.
Location/Qualifiers
1..675

FEATURES
source


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/organism="Drosophila melanogaster"
/mol_type="mrna"
/db_xref="taxon:7227"
/clone="GH08678"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pot2"
/note="Organ: head; Vector: pot2; Site: 1: ECORI; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated into
pot2. Plasmid cDNA library."

```

ORIGIN

	Query Match	6.0%;	Score 216.4;	DB 9;	Length 675;
	Best Local Similarity	58.9%;	Pred. No. 1.8e-39;		
	Matches 392;	Conservative	0;	Mismatches 271;	Indels 3;
				Gaps	1;
Qy	1719	ACTGCCACGGTTC	CCGTGACCGCCTGAAGCAGCTTGGCCAGCCGCTTGCCTCGTGA	1778	
Db	8	ACCACGAAAGGACT	CCGCGAGGTCTTGTTGCGAAGGTCCGGAGGCCCTTCGCCAAGGA	67	
Qy	1779	TCTCCGTGAGCAGC	AGCAGTGGCAGTTACTGATACCACTTCCGCGATGCACACCAAGTC	1838	
Db	68	GGTGGCAACCGTA	AGGAACCTGCTACTCATGGACACCACTTCCGCGATGCCACCAAGTC	127	
Qy	1839	TTTGCCTTGGACCC	GAGTCCGCTCATTCGCACCTGAAGCCTGGGCGAGGCCGTCGCAAA	1898	
Db	128	GCTGCTGGCCACC	CGCGTGCCTTCCACGATCTGCTGAAGATCTCCCCCTACGTGACGCA	187	
Qy	1899	GCTGACTCCTGAGC	TTTGTCCGTTGGAGGCCCTGGGCGGCGCGACCTACGATGTGGCGAT	1958	
Db	188	CAAGTTCAACAAC	CTGTATTGCTGGAGAACTGGGGCGGAGCCACCTTCGACGTGGCGCT	247	
Qy	1959	GCGTTTCCTCTTT	GAGGATCCGTTGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAA	2018	
Db	248	GCGCTTCCTGAC	GAGTGCCCGTGGGAGCGCTTGAGGAGATGCGCAAGCGCATCCCGAA	307	
Qy	2019	TGTAACAATT	CAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACCCCGTACCCAGA	2078	
Db	308	CATTCCCTTCCAG	ATGCTGTTGCGCGGAGCCACCGCTCGGCTACACCAAGCTATCCGGA	367	
Qy	2079	CTCCGCTCTGCG	CGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCTAT	2138	
Db	368	CAACGTGGTCTA	CAAGTTCTGTGAGCTGGCTGTGTCAGACCGGCATGGACATCTTCAGGGT	427	
Qy	2139	CTTCGACCGGCTT	AAACGACGTCTCCAGATGCGTCCAGCAATCGACGCGAGTCTCTGGAGAC	2198	
Db	428	GTTCGACTCGCT	CAACTACCTGCCAACCTGATCTCTCGGCATGGAAGCCGCTGGAAGGC	487	
Qy	2199	CAACACCGCGGT	AGCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGA	2258	
Db	488	GGGCGGCGTGGT	---GGAGGCTGCCATCTCCTATACCGGAGACGTGAGCGATCCCAAGCG	544	
Qy	2259	AAAGCTCTACAC	CCCTGGATTACTACCTAAAGATGCGAGAGGAGATCGTCAAGTCTGGCGC	2318	
Db	545	CACCAAGTATGAT	CTGAAATACTACACTAACCTTGGCGATGAGCTGGTCAAGGCGGGCAC	604	
Qy	2319	TCACATCTTGG	CCATTAAAGGATATGGCTGGTCTGCTTCGCCAGCTGCGGTAACCAAGCT	2378	
Db	605	CCACGTGCTCTG	CATAAAGGATATGGCTGGTCTGCTCAAGCCCGAATCCGCCAGGCTTCT	664	
Qy	2379	GGTCAAC	2384		
Db	665	GATCAC	670		

RESULT 11
BI103175
LOCUS
DEFINITION
BI103175 744 bp mRNA linear EST 26-JUN-2001
602889415F1 NCI CGAP_Kidl4 Mus musculus cDNA clone IMAGE:5044779
5', mRNA sequence.
ACCESSION
VERSION
BI103175.1 GI:14554068

EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 744)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1122 row: m column: 04
High quality sequence stop: 737.
Location/Qualifiers
1. .744
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5044779"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library. |"

ORIGIN

Query Match	5.9%;	Score 214.8;	DB 12;	Length 744;
Best Local Similarity	58.6%;	Pred. No. 4.e-39;		
Matches 430;	Conservative	0;	Mismatches 297;	Indels 7; Gaps 3;
QY	1765	GC GTT TGC TGT GAT C T CCG T GAG CAG GAC GCA C TGG CAG T TACT GAT ACC AC CTT TCC GC	1824	
Db	15	GGG CTT GCC GAG C TGT GCG GAATC ACC AC GGG C TGT GTT GAT GG AC ACA C CTT TCC GG	74	
QY	1825	GAT G CAC ACC AGT C TTT GCT TGC GAC CCG AGT CCG C TCA TT CG CACT GA AG C CTG CGG CA	1884	
Db	75	GAT GCC CAC CAG T CACT ACT TGG CCA C TAG AGT GCG CAC ACAT GAT CT CAA - AAAG ATCG	133	
QY	1885	GAG GCC GTG CCA AAG CTG ACT CCT GAG C TTT GT CCG TGG AGG C CTTGGG GCG CGC GACC	1944	
Db	134	CCCT ATG TTGCC CACA CA CTTTCAA CAAG CTCTT CAG CATGG AGA ACTGGG GAG CGCCACG	193	
QY	1945	TAC GATG TGG CGATG CG TTTCC TCTTTGAGGATCCG TGGGACAGGCTCGACGAGCTGCGC	2004	
Db	194	TTCGACGTTGCCATGCGCTTCC TGTACAGTGC C C C TGGCGGCGCTCCAGGAGCTCCGG	253	
QY	2005	GAGGCGATGCCGAATGTAA CATT CAGATGCTGCTTCGCGGCCGCAACACCGTGGGATAC	2064	
Db	254	GAGCTTATCCGGAACATCCCGTTCCAGATGCTACTGAGGGGGCCCAATGCTGTGGGTAC	313	
QY	2065	ACCCCGTACCAGACTCCGTCTGCGCGCGCTTGTTAAGGAAGCTGCCAGTCCGGCGTG	2124	
Db	314	ACCAACTACCTTGACAACGTGGTCTTCAAGTCTGTGAGGTGGCCAAAGAGAATGGTATG	373	
QY	2125	GACATCTTCCGATCTTTCGACGGCTTAACGACGTCTCCCAGATCGTCCAGCAATCGAC	2184	
Db	374	GACGCTTCCGAGCTTTGACTCCCTCAACTACTTGGCCAAACATGCTGCTGGSCATGGAA	433	
QY	2185	GCAGTCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGTGTATCTC	2244	
Db	434	GCAG-- -CAGSCAGTCTGGGGGTGTGGTGGAGGCTGCCATCTCATACACGGGGGACGTG	490	
QY	2245	TCTGATCCAAATGAAAAGCTCTACACCCCTGGATTACTACCTAAAGATGGCAGAGGAGATC	2304	

Db 491 GCTGACCTAGTCGCACCTAAATACTCACTGGAGTACTACATGGGCTTAGCTGAAGAACTG 550

Qy 2305 GTCAAGTCTGGCGCTCACAATCTTGCCATTAAAGGATATGGCTGGTCTGTCTTCGCCAGCT 2364

Db 551 GTGCGAGCTGGCACTCACAATCTTGCCATTAAAGGATATGGCGGCTGTCTGAAGCTGCC 610

Qy 2365 GCGGTAAACCAAGCTGGTCAACCGACTCGG---CCGTGAATTCGATCTGCCAGTGCAGTG 2421

Db 611 GCCTGACCATGCTGGTCACTCCCTCCGGGACCGATTCCCGACCTCCCACTGCACATC 670

Qy 2422 CACACCCACGACACTGCGGGTGGCCAGCTGGCAACCTACTTTGCTGCAGCTCAAGTGGT 2481

Db 671 CATACCCATGATACATCAGGGGCGAGGTGGCAGCCATGCTGGCCTGTGCACAAGCAGGG 730

Qy 2482 GCAGATGCTGTTGA 2495

Db 731 GCTGATGCTGTGA 744

RESULT 12

LOCUS CK000115

DEFINITION AGENCOURT 16368972 NIH_MGC 220 Homo sapiens cDNA clone

IMAGE:30707731 5', mRNA sequence.

ACCESSION CK000115

VERSION CK000115.1 GI:38526149

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 800)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Martin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM1072 row: m column: 20

High quality sequence start: 12

High quality sequence stop: 654.

High quality Location/Qualifiers

FEATURES

source

1..800

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30707731"

/lab_host="DH10B Tona"

/clone_lib="NIH MGC 220"

/note="Organ: mixed; Vector: pYX-Asc; Site 1: EcoRI; Site 2: NotI; Library is oligo-dT primed and directionally cloned Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. Average insert size 0.5-1kb. Adaptors 5' (AATTCGGCAGGAGG)3' and 5'd (CTCGTGGCCG)3' 3' Linker sequence - GCGGCCGTGAGAGCC T18. Sequencing primers 3'end: T3 promoter primer 5'd (ATTAACCTCACTAAAGGA)3' 5' End: T7 promoter primer 5'd (TAATACGACTACTATAGGG)3' 3' Library was constructed in the laboratory of M. Bento Soares. Average insert size 3-4kb

Note: this is a NIH_MGC Library."

ORIGIN

Query Match 5.9%; Score 213.2; DB 14; Length 800;

Best Local Similarity 59.1%; Pred. No. 1.1e-38;

Matches 401; Conservative 0; Mismatches 273; Indels 4; Gaps 2;

Qy 841 AACCTCAGCATATTGAAGTGCAG-ATCCTTGGCGATCAGTGGAGAGTTGTACACCT 899

Db 35 AAGCCACGGCACATCGAGGTGAGAATCTTGGGGGACCAAGTATGGGAACATCTCTGCACCT 94

Qy 900 TTATGAACGTGACTGCTCACTGACGCGTCTGCACCAAAAAGTTGTGCAAAATTCGCCCAGC 959

Db 95 GTACGAGCGAGACTGCTCCATCCAGCGCGGCACACAGAGGTGGTGCAGATTGCCCCCGC 154

Qy 960 ACAGCATTTGGATCCAGAACTGCGTATCGCATTTGTGCGGATGCAGTAAAGTTCTGCGG 1019

Db 155 CGCCCACTGGACCCGAGCTTCGGACTCGGCTCACAGCGACTCTGTGAAACTCGCTAA 214

Qy 1020 CTCCATTGTTACCAGGGCGGGGAAACCGTATCCAGTGGAAATCTTGGTTCGATGAAAGGCAACCA 1079

Db 215 ACAGGTGGGCTACGAGAACCGAGGACCGTGGAGTTCTTGTGGACAGGCACGGCAAGCA 274

Qy 1080 CGTCTTCATCGAAATGAACCCACGATATCCAGTGGAGCACACCGTGCAGTACGAGAGTCAAC 1139

Db 275 CTACTTTCATCGAGGTCAACTCCCGCTGCAGGTGGAGCACACCGTGCAGTACCGGTCAACCA 334

Qy 1140 CGAGGTGGACCTGGTGAAGCGCGAGATCGGCTTGGCTGCTGTGTCAACTTGAAGGAATT 1199

Db 335 CGACGTAGACCTGGTCCATGCTCAGATCCACGTGGTGAAGGAGGAGGCTTACCCGACCT 394

Qy 1200 GGGTCTGACCCCAAGATAAGATCAAGACCCACCGTGCAGCATCTGCAGTGCCTCACC 1259

Db 395 GGGCTGCGGCGAGGAGAACATCCGCTATCAACCGGTGTGCCATCCAGTGCCTGGTCAACCA 454

Qy 1260 GGAAGATCCAAACAAACGGCTTCCGCCAGATACCGGAACATATCACCGGTACCGTCAAC 1319

Db 455 CGAGGACCCCGCGCGAGCTTCCAGCGCGACACCGCGCATTTGAGGTGTTCCGGAGCGG 514

Qy 1320 AGCGGAGCTGGCTTCGTCT--TGACGGTGCAGTCCAGTCCGGTGGCGGAAATCACCGC 1376

Db 515 AGAGGGCATGGGCTCCGCTGGATAATGTTCCGCTTCCAGGAGCGCTCATCTCGCC 574

Qy 1377 ACACCTTGAATCCATGCTGGTGAATAATGACCTGCGTGGTTCGACTTTGAAACTGTGT 1436

Db 575 CCACTACGACTCCCTGCTGGTCAAGTCAATTCGCCACGGCAAGACCAACCCACGGCGCG 634

Qy 1437 TGCTCGTGCACAGCGCGCTTGGTGGTGGTTCACCGTGTCTGTGGTGTGCAACCAACATTGG 1496

Db 635 CACCAAGATGAGCAGGGCCCTTGGGAGTTCGCGTCCGAGGTGTGAGACCAACATCGC 694

Qy 1497 TTTCTTGGCTGGCTTGTCT 1514

Db 695 CTTCCTGCAGAAATGTGCT 712

RESULT 13

BI618593

LOCUS

DEFINITION BI618593.1 640 bp mRNA linear EST 07-SEP-2001

DESCRIPTION RH49459.5prime RH Drosophila melanogaster normalized Head pFLC-1

Drosophila melanogaster cDNA clone RH49459 5 similar to

BCDNA:GH06348: FBan0001516 GO:[pyruvate carboxylase (GO:0004736)]

located on: 2R 46B14-46C1; 08/19/2001, mRNA sequence.

BI618593

BI618593.1 GI:15514118

EST.

KEYWORDS Drosophila melanogaster (fruit fly)

SOURCE Drosophila melanogaster

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 640)

REFERENCE Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E.,

George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G.,
Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and
Rubin,G.M.
BDGP/HMI RH Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
hit genomic AB003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46E4: 08/19/2001
Plate: RH.494 row: E column: 11
High quality sequence stop: 543.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RH49459"
/sex="male and female"
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/clone_lib="RH Drosophila melanogaster normalized Head
pFlc-1"
/note="Organ: head; Vector: pFlc1; Site 1: XhoI; Site 2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
ORIGIN
Query Match 5.8%; Score 211; DB 12; Length 640;
Best Local Similarity 59.4%; Pred. No. 3.2e-38;
Matches 377; Conservative 0; Mismatches 255; Indels 3; Gaps 1;
QY 790 GCTGAACGGCGCTTTGGCGATGGCGGGTATATGTGAACGTGCTGTGATTAACCCCTCAG 849
Db 1 GCCAAGCGCGCTTTGGCAATGGTGGATGTTCAATTGAGAAGTTCATCGAGCGCACCGCGT 60
QY 850 CATATTGAAGTGCAGATCCCTTGGCGATCACACTGGAGAAGTTGTACACCTTTATGAACGT 909
Db 61 CACATTGAGGTTCAACTGCTGGAGACAAGCGCGGGAATGTAGTGCACTGTACGAACGT 120
QY 910 GACTGCTCACTGACGCGTGTGTCACCAAAAGTTGTGAAATTCGCCAGCACAGCATTTG 969
Db 121 GACTGCTCGTGCAGCGTGCACCAAGAGGTTGGTGGAGATCGCCCCAGCGCCACGCTG 180
QY 970 GATCAGAACTGCGTGATCGCAATTTGTGCGGATGAGTAAAGTTCTGCCGCTCCATTTGGT 1029
Db 181 CCAATCGAAATCCGGACAAGATGACGGAGGCAGCATGCGCTTGGCCCGCCATGTGGGC 240
QY 1030 TACCAGGCGCGGGAAACCGTGGAAATCTTGGTCGATGAAGGCAACCAACGCTTTCATC 1089
Db 241 TATGAAACGCGCGGAACCGTGGAGTTCCTTTGCGACGAGTCCGGCAACTTCTACTTCATC 300
QY 1090 GAATGAACCCACGATATCCAGGTTGAGCACACCGTGACTGAAGAAAGTCAACCGAGGTGGAC 1149
Db 301 GAAGTGAACGCCCGTCTACAAGTGGAGCACACCGTCAACGAGGAGATAACAGGCATCGAT 360
QY 1150 CTGGTGAAGGCGCAGATGCGCTTGGCTGTGGTGCAACCTTGAAGGAATTTGGTGTGACC 1209
Db 361 TTGGTGCAGTCGCAATCCCGGTGGCGGAGGCATGACCCATCCGAAATTTGGGCTACACG 420
QY 1210 CAAGATAAGATCAAGACCCACCGTGCAGCACTGCAGTGGCGCATCACCAACGGAAGATCCA 1269
Db 421 CAGGACAAGATCGTCCCGGTGGCTATGCCATTGAGTGGCGGTGACCAACCGAAGATCCG 480
QY 1270 AACACGGCTTCCGCCCAGATACCGGAACATATCACCGGTACCGCTCACCAAGCGGAGCT 1329
Db 481 GCCAACGATTTTCAGCCCAACACCGGTGCTTGGAGGTCTTCCGATCTGGCGAGGGTATG 540

1330 GCGGTTCTGTTACGGTG---CAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGAC 1386
Db 541 GGCATTAGGTTGGACAGTGGTCCGCTTACCGCGGAGCCATCATTTCCCATACTACGAC 600
QY 1387 TCCATGCTGGTGAATAATGACCTGCCGTGGTTCCGA 1421
Db 601 TCCCTGCTGGTCAAGTGATCTCGCACGCCACGCA 635
RESULT 14
BG910468
LOCUS
DEFINITION BG910468 715 bp mRNA linear EST 05-JUN-2001
602806142F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4938203
5', mRNA sequence.
ACCESSION BG910468
VERSION BG910468.1 GI:14290944
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 715)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10873 row: d column: 12
High quality sequence stop: 715.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:4938203"
/tissue_type="anaplastic oligodendroglioma with lp/19q
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 5.7%; Score 208.2; DB 12; Length 715;
Best Local Similarity 56.8%; Pred. No. 1.5e-37;
Matches 403; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
QY 872 GCGATCACACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTCGTC 931
Db 1 GGGACCATATGGGAACATCTCTGCACCTGTACGAGCGAGACTGCTCCATCCAGCGCGGC 60
QY 932 ACCAAAAAGTTGCGAAATTCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCA 991
Db 61 ACCAGAAGTGGTTCGAGATTGCCCGCCCGCCACCTGGACCCGAGCTTCGGACTCGGC 120
QY 992 TTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGAACCGTGG 1051
Db 121 TCACCAGCGACTCTGTGAAACTCGTAAACAGGTGGGTACGAGAACGAGGACCGGTGG 180
QY 1052 AATTCTTGGTCGATGAAAGGGCAACCAACGCTCTTCATCGAAATGAACCCACGTATCCAGG 1111
Db 181 AGTTCCTGTTGGACAGGACCGCAAGCACTACTTCATCGAGGTCACTCCCGCTGCAGG 240
QY 1112 TTGAGCACACCGTGACTGAAGAAGTCAACGAGGTGGACCTGGTGAAGGCGCAGATGCGCT 1171

Db 241 TGGAGCACACGGTACAGAGGAGATCACCGAGTAGACCTGGTCCATGCTCAGATCCACG 300
QY 1172 TGGCTGCTGGTGAACCTTGAAGGAATTTGGGTCTGACCCCAAGATAAGATCAAGACCCACG 1231
Db 301 TGGCTGAGGGCAGGAGCCTACCCGACCTGGGCTCGGCAGGAGAACATCCGCATCAACG 360
QY 1232 GTGCAGCACTGCAGTCCGCGATCACCAAGGAGATCCAAACAACGGCTTCCGCCAGATA 1291
Db 361 GGTGTGCCATCCAGTCCGGGTCAACCAAGGAGACCCCGCGGCGAGCTTCCAGCCGGACA 420
QY 1292 CCGGAACATATCACCGCGTACCGCTCAACAGCGGAGCTGGCGTTCGTTCTTGACGGTGCAG 1351
Db 421 CCGGCCGATTTAGGTGTTCCGGAGCGGAGGGGCATGGGCATCCGCTGGATAATGCTT 480
QY 1352 CTCAGCTC---GGTGGCGAAATCACCGGACACTTTGACTCCATGCTGGTGAAGATGACCT 1408
Db 481 CCGCTTCCAGGAGCCGTCTATCTCGCCCACTACGACTCCCTGCTGCTCAAGTCAATTG 540
QY 1409 GCCGTGGTCCGACTTTGAAACTGCTGTGCTGTCGACAGCGCGCTTGGCTGAGTTCA 1468
Db 541 CCACGGCAAAGACCAACCCAGCGCGCCCAAGATGAGCAGGGCCCTTGGGAGTTCC 600
QY 1469 CCGTGTCTGGTGTGCAACCAACATTTGTTCTTTCGCTGCGTTCGCGGAGAGGACT 1528
Db 601 GCGTCCGAGGTGTGAAGACCAACATCGCTCTCTGCGAATGTGCTCAACACCGCACT 660
QY 1529 TCACCTCCAGCGCATCGCCACCGGATTCATTCGCGATCACCCGACCT 1577
Db 661 TCCTGGCAGGCACTGTGGACACCAGTTTCATCGACGCGAGAACCCAGACT 709

RESULT 15
BJ063722 641 bp mRNA linear EST 29-SEP-2003
LOCUS BJ063722 NIBB Mochii normalized Xenopus tailbud library Xenopus
DEFINITION laevis cDNA clone XL077c10 5', mRNA sequence.
ACCESSION BJ063722
VERSION BJ063722.1 GI:17470882
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 641)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following URL.
http://xenopus.nibb.ac.jp.
Location/Qualifiers
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ORIGIN

Query Match

5.6%; Score 204.4; DB 12; Length 641;

Best Local Similarity 58.9%; Pred. No. 1.1e-36;
Matches 371; Conservative 0; Mismatches 256; Indels 3; Gaps 1;
QY 841 AACCTCAGCATATTGAAGTGCAGATCTTGGCGCATCACACTGGAGAAGTTGTACACCTT 900
Db 5 AAACCTCGCCACATTGAAGTTTCAGATACTCGGTGATAAATATGGAATGTGGTACATTG 64
QY 901 TATGAACGTGCTGCTCAGTGCAGCGTGTGTCACCAAAAGTTGTGCGGATGAGTAAAGTTCTGCCGC 960
Db 65 TATGAAGAGACTGTTCCGTCCAGAGAAGCCACAGAGGTGGTTGAAATAGCCCCAGCT 124
QY 961 CAGCATTTGGATCCAGAACTGCGTGTATCGCATTTGTGCGGATGAGTAAAGTTCTGCCGC 1020
Db 125 GCACAGCTGGACCTTCAGCTCAGAGACAGACTGACCCATGACTCTGTAAAACTGGCAAAA 184
QY 1021 TCCATTGGTTACAGGGCGCGGAAACCGTGGAAATCTTGGTCCGATGAAAGGGCAACAC 1080
Db 185 CAGGTGGTTATGAGAAATGCCGGCACTGTGGAGTTCTTGGTGATFAAACATGGCAAGCAT 244
QY 1081 GTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGAAGTCAAC 1140
Db 245 TACTTCATAGAAGTCAACTCCAGACTCCAAAGTTGAGCATACAGTAACGGAAGAAATTACA 304
QY 1141 GAGGTGACCTGCTGGAAGCGCGAGATCGCTTGGTGTGCAACCTTGAAGGAATTG 1200
Db 305 GATGTTGACCTAGTCCATGCCCGATCCATGTTGCAGAGGGGAAAAGCCTTCTCTGACCTT 364
QY 1201 GGTCTGACCCAGATAAGATCAAGACCCACCGTGCAGCACTGCGAGTCCGCGCATCACCG 1260
Db 365 GGCCTCAAGCAAGAGAACATCCGTATCAATGGTTGTGCCATTTCAGTGCAGAGTCAACA 424
QY 1261 GAAGATCCAAACAACGGCTTCCGCCAGATACCGGAACATATCACCGGTACCGCTCACCA 1320
Db 425 GAAGACCTTCACGTGGGTTTCAGCCTGATACCTGGTGGATTGAGGTTTCCGGAGTGA 484
QY 1321 GCGCGAGCTGGCTGCTGTTGACGGTG--CAGCTCAGCTCGGTGGCGAAATCACCGCA 1377
Db 485 GAAGGAATGGGAATCCGACTAGACAGTGTTCAGCTTTTCAAGGAGCTGTCTATTTCCCA 544
QY 1378 CACTTTGACTCCATGCTGGTGAATGACCTGCCGTGGTTCCGACTTTGAAACTGCTGTT 1437
Db 545 CATTATGACTCCCTTCTGGTCAAGGTATTGACACCGGAAAAGACCATCAAGTTGCCGCC 604
QY 1438 GCTCGTGCACAGCGCGCTTGGCTGAGTTC 1467
Db 605 ACAAAAATGACGACAGAGCTTTGGCAGAGTTC 634

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Job time : 8678 secs